

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 10:08:02 ; Search time 33.0612 Seconds
(without alignments)
1717.821 Million cell updates/sec

Title: US-09-905-666A-75
Perfect score: 939
Sequence: 1 EHNPFVVMHGIGASNFAG.....NSQVNSLIKEGLNGGLNTN 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:**

- 1: sp_archaea:**
- 2: sp_bacteria:**
- 3: sp_fungi:**
- 4: sp_human:**
- 5: sp_invertebrate:**
- 6: sp_mammal:**
- 7: sp_muc:**
- 8: sp_organelle:**
- 9: sp_phase:**
- 10: sp_plant:**
- 11: sp_rodent:**
- 12: sp_virus:**
- 13: sp_vertebrate:**
- 14: sp_unclassified:**
- 15: sp_rvirus:**
- 16: sp_bacteriap:**
- 17: sp_archaeap:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	746	79.4	181	2 Q9K5F4	Q9K5F4 bacillus li
2	733	78.1	215	2 Q8VU78	Q8VU78 bacillus sp
3	714	76.0	210	16 P94444	P94444 bacillus sp
4	702	74.8	210	2 Q8RJP5	Q8RJP5 bacillus me
5	431	45.9	201	2 Q83VD0	Q83VD0 paenibacill
6	202	21.5	228	16 Q82676	Q82676 streptomyce
7	193.5	20.6	286	16 Q828V2	Q828V2 streptomyce
8	193	20.6	237	16 Q8RSF6	Q8RSF6 deinococcus
9	180.5	19.2	331	16 Q9K165	Q9K165 streptomyce
10	172.5	18.4	286	16 Q82HF7	Q82HF7 streptomyce
11	170	18.1	290	16 Q8S295	Q8S295 streptomyce
12	168	17.9	403	16 Q8RC93	Q8RC93 thermococyst
13	156.5	16.7	202	16 P73372	P73372 corynebacte
14	156	16.6	324	16 Q8NU60	Q8NU60 corynebacte
15	150.5	16.0	339	2 Q59644	Q59644 propionibac
16	149	15.9	352	16 Q8FUC7	Q8FUC7 corynebacte

17	147.5	15.7	275	2	O33969	O33969 streptomyce
18	145.5	15.5	289	16	Q9K3H5	Q9K3H5 streptomyce
19	144	15.3	211	16	O8YX63	O8YX63 anabaena sp
20	140	14.9	291	14	Q91UY0	Q91UY0 uncultured
21	134.5	14.3	300	5	Q19310	Q19310 caenorhabdi
22	134.5	14.3	371	5	Q22420	Q22420 caenorhabdi
23	133.5	14.2	549	16	Q8FUC6	Q8FUC6 corynebacte
24	133	14.2	286	5	Q9NAK4	Q9NAK4 caenorhabdi
25	130.5	13.9	344	5	Q23548	Q23548 caenorhabdi
26	130	13.8	300	16	Q8NU59	Q8NU59 corynebacte
27	126	13.4	479	16	Q97K91	Q97K91 clostridium
28	122.5	13.0	339	16	O8XXN1	O8XXN1 ralstonia s
29	121.5	12.9	266	16	O8R9R3	O8R9R3 bradyrhizob
30	121	12.9	271	16	O8ERS5	O8ERS5 ocanobacil
31	121	12.9	292	5	O76556	O76556 caenorhabdi
32	120.5	12.8	474	17	O28511	O28511 archaeoglob
33	118	12.6	197	16	Q7V291	Q7V291 prochloroco
34	117.5	12.5	360	2	O68551	O68551 pseudomonas
35	116	12.4	335	5	O17622	O17622 caenorhabdi
36	116	12.4	340	5	O16380	O16380 caenorhabdi
37	115.5	12.3	290	2	Q52614	Q52614 proteus vul
38	115	12.2	171	2	Q56594	Q56594 vibrio chol
39	115	12.2	333	5	Q20437	Q20437 caenorhabdi
40	113	12.0	190	2	Q832V1	Q832V1 bacillus su
41	112.5	12.0	300	16	Q92D71	Q92D71 listeria in
42	112	11.9	380	2	Q31909	Q31909 pseudomonas
43	110.5	11.8	329	5	Q22060	Q22060 caenorhabdi
44	110	11.7	309	2	P72172	P72172 pseudomonas
45	110	11.7	309	16	Q9HUZ7	Q9HUZ7 pseudomonas

ALIGNMENTS

RESULT 1

Q9K5F4	ID	Q9K5F4	PRELIMINARY;	PRT;	181 AA.
AC	O9KGF4;	AC	O9KGF4;		
DT	01-OCT-2000 (Tremblrel. 15, Created)	DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)		
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)	DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)		
DE	Lipase (EC 3.1.1.3) (Fragment).	DE	Lipase (EC 3.1.1.3) (Fragment).		
OS	Bacillus licheniformis.	OS	Bacillus licheniformis.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1402;	OX	NCBI_TaxID=1402;		
RN	[1]_TaxID=1402;	RN	[1]_TaxID=1402;		
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.		
RX	PubMed=11339956;	RX	PubMed=11339956;		
RA	Nthangeni M.B., Patterson H.G., Van Tonder A., Vergeer W.P.,	RA	Nthangeni M.B., Patterson H.G., Van Tonder A., Vergeer W.P.,		
RA	Litthauer D.;	RA	Litthauer D.;		
RT	"Over-expression and properties of a purified recombinant Bacillus	RT	"Over-expression and properties of a purified recombinant Bacillus		
RL	licheniformis lipase: a comparative report on Bacillus lipases.";	RL	licheniformis lipase: a comparative report on Bacillus lipases.";		
RL	Enzyme Microb. Technol. 28:705-712(2001).	RL	Enzyme Microb. Technol. 28:705-712(2001).		
DR	EMBL; AJ297356; CAB95850.1; -	DR	EMBL; AJ297356; CAB95850.1; -		
DR	GO; GO:0016787; F:hydrolase activity; IEA.	DR	GO; GO:0016787; F:hydrolase activity; IEA.		
DR	GO; GO:0004806; F:triacylglycerol lipase activity; IEA.	DR	GO; GO:0004806; F:triacylglycerol lipase activity; IEA.		
DR	GO; GO:0016042; P:lipid catabolism; IEA.	DR	GO; GO:0016042; P:lipid catabolism; IEA.		
DR	InterPro; IPR002918; Ser esters.	DR	InterPro; IPR002918; Ser esters.		
DR	Pham; PF01674; Lipase_2; 1.	DR	Pham; PF01674; Lipase_2; 1.		
KW	Hydrolase.	KW	Hydrolase.		
FT	NON_TER	FT	NON_TER		
SQ	SEQUENCE 181 AA; 19220 MW; 04D2AD28D3B0BB8 CRC64;	SQ	SEQUENCE 181 AA; 19220 MW; 04D2AD28D3B0BB8 CRC64;		

Query Match 79.4%; Score 746; DB 2; Length 181;

Best Local Similarity 78.3%; Pred. No. 2.8e-51;

Matches 141; Conservative 17; Mismatches 22; Indels 0; Gaps 0;

Qy	1	EHNPFVVMHGIGASNFAGISYLVSCSRGKLYAVDFDKTGTNNYNGPVLSEFKK	60
Db	2	EHNPFVVMHGIGASNFASIKSYLVGGQWDRNQLFAIDFDKGTNNRNGPRLSFKVD	61
Qy	61	VLDETCAKKVDIVAHSGMGANTLYIKNLDDGKNVENVTLGCTNRSTTSKALPGTDPNQ	120

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Db 62 VLDKTKAKKVDIVAHSMGGANTLYIKNLGGDKIENVVIGGANGLVSSRA,PGTDPNQ 121
Qy 121 KILYTSYSSADMIVMNYLSKLDGAKVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
Db 122 KILYTSYSSADLIVVNSLSRLGARNVLIHGVLGHIGLLTSSQVKYVKEGLNGGQNTN 181

RESULT 2
Q8VU78 PRELIMINARY; PRT; 215 AA.
AC 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Lipase.
OS Bacillus sp. B26.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=117494;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B26;
RA Kim M.H., Kim H.K., Oh T.K., Lee J.K.;
RT "Cloning and sequencing of a lipase gene from Bacillus sp. B26.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF232707; AAL36938.1; -.
DR GO; GO:0003824; P: catalytic activity; IEA.
DR GO; GO:0016298; P: lipase activity; IEA.
DR GO; GO:0016042; P: lipid catabolism; IEA.
DR InterPro; IPR002918; Lipase 2.
DR InterPro; IPR000379; Ser_eatrs.
DR Pfam; PF01674; Lipase 2; 1.
SQ SEQUENCE 215 AA; 22959 MW; 460397D7026A789B CRC64;

Query Match 78.1%; Score 733; DB 2; Length 215;
Best Local Similarity 77.2%; Pred. No. 3.8e-50;
Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;

Qy 1 EHNPMVVMHVGIGGASFNAGIKSVLSQSGWGRKLYAVFDWKTGTNNYNGPVLSPVKK 60
Db 36 EHNPMVVMHVGIGGASFNAGIKSVLSQSGWQDQNLFAIDFKTGNLNGPRLSRVKD 95

Qy 61 VLDKTKAKKVDIVAHSMGGANTLYIKNLGGDKIENVVIGGANGLVSSRA,PGTDPNQ 120
Db 96 VLAKTGAKKVDIVAHSMGGANTLYIKNLGGDKIENVVIGGANGLVSSRA,PGTDPNQ 155

Qy 121 KILYTSYSSADMIVMNYLSKLDGAKVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
Db 156 KILYTSYSSADLIVVNSLSRLGARNVLIHGVLGHIGLLTSSQVKYVKEGLNGGQNTN 215

RESULT 3
P94444 PRELIMINARY; PRT; 210 AA.
AC P94444;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Extracellular esterase precursor (EC 3.1.1.1) (Yfip).
GN LIPA OR LIPE.
OS Bacillus sp. BP-6, and
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=187867; 1423;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Bacillus sp. BP-6; STRAIN=BP-6;
RA Ruiz C., Pastor J., Diaz P.;
RT "Identification and cloning of Bacillus megaterium and Bacillus sp.
RT BP-6 esterases. Comparison with Bacillus subtilis and Bacillus pumilus
RT lipases.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
```

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RP SEQUENCE FROM N.A.
RC SPECIES=B.subtilis; STRAIN=AC327;
RX MEDLINE=97128783; PubMed=8973323;
RA Yamamoto H., Uchiyama S., Sekiguchi J.;
RT "The Bacillus subtilis chromosome region near 78 degrees contains the
RT genes encoding a new two-component system, three ABC transporters and
RT a lipase.";
RL Gene 181:147-151 (1996).
RN [3]

SEQUENCE FROM N.A.
RC SPECIES=B.subtilis; STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grand G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Fujic P., Purnelle B., Rapoport G., Ray M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256 (1997).
RN [4]

SEQUENCE FROM N.A.
RC SPECIES=B.subtilis; STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ430985; CAD24006.1; -.
DR EMBL; D78508; BAA11406.1; -.
DR EMBL; Z98108; CAB12664.1; -.
DR FIR; C69652; C69652.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0016298; F:lipase activity; IEA.
DR GO; GO:0004759; F:serine esterase activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR002918; Lipase 2.
DR InterPro; IPR000379; Ser_eatrs.
DR Pfam; PF01674; Lipase 2; 1.
KW Hydrolase; Signal; Complete proteome.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 1 210 EXTRACELLULAR ESTERASE.
SQ SEQUENCE 210 AA; 22363 MW; 4359843F882C690A CRC64;

Query Match 76.0%; Score 714; DB 16; Length 210;
Best Local Similarity 74.3%; Pred. No. 1.2e-48;
Matches 133; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

Qy 2 HNPVVMHVGIGASFNAGIKSVLSQSGWGRKLYAVDFWKTGTNNYNGPVLSPVKY 61
Db 32 HNPVLMVHGIGASYNFPAIKNYLISQGWQSKLYAIDFYDKTGNLNGPQLASYDVR 91

Qy 62 LDSTGAKKVDIVAHSMGGANTLYIKNLGGDKIENVVIGGANGLVSSRA,PGTDPNQ 121
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Db 92 LKETGAKKVDIVAHSMGGANTLYIKYLGGNKIQNVTLGGANGLVSTALPGTDPNQK 151
QY 122 ILVTSYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
Db 152 ILVTSYSLNDQIVNSLSRQAGNIQLYGIGHIGLLNSQVNGYIKKEGLNGGLNTN 210

RESULT 4
Q8RUP5 PRELIMINARY; PRT; 210 AA.
AC Q8RUP5;
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Extracellular esterase precursor (EC 3.1.1.1).
GN LIPA.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC3985;
RA Ruiz C., Pastor J., Diaz P.;
RT "Identification and cloning of Bacillus megaterium and Bacillus sp.
RT BP-6 esterases. Comparison with Bacillus subtilis and Bacillus pumilus
RT lipases.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ430831; CAD23620.1; -.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0016298; F:lipase activity; IEA.
DR GO: GO:0004759; F:serine esterase activity; IEA.
DR GO: GO:0016042; F:lipid catabolism; IEA.
DR InterPro: IPR002918; Ser_estrs.
DR Pfam: PF01674; Lipase_2; 1.
DR Signal; Hydrolase.
KW SIGNAL.
FT CHAIN
FT CHAIN
SQ SEQUENCE 210 AA; 22411 MW; 9408989882C6918 CRC64;

Query Match 74.8%; Score 702; DB 2; Length 210;
Best Local Similarity 73.2%; Pred. No. 1e-47;
Matches 131; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 2 HNPVVMVHGIGGASFNAGIKSYLVSGWSRGKLYAVDFWDKTGTNNYNGPVLRSFVKV 61
Db 32 HNPVLMVHGIGGASFNAGIKSYLVSGWSRGKLYAVDFWDKTGTNNYNGPQLASYVDRV 91
QY 62 LDETGAKKVDIVAHSMGGANTLYIKYKLDGKNVENVVTLGGTNRSTTSKALPGTDPNQK 121
Db 92 LKETGAKKVDIVAHSMGGANTLYIKYLGGNKIQNVTLGGANGLVSTALPGTDPNQK 151
QY 122 ILVTSYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
Db 152 ILVTSYSLNDQIVNSLSRQAGNIQLYGIGHIGLLNSQVNGYIKKEGLNGGLNTN 210

RESULT 5
Q83VDO PRELIMINARY; PRT; 201 AA.
AC Q83VDO;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE PLA depolymerase.
GN PLA.
OS Paenibacillus amylolyticus.
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxID=1451;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TB-13;

Query Match 74.8%; Score 702; DB 2; Length 210;
Best Local Similarity 73.2%; Pred. No. 1e-47;
Matches 131; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 2 HNPVVMVHGIGGASFNAGIKSYLVSGWSRGKLYAVDFWDKTGTNNYNGPVLRSFVKV 61
Db 32 HNPVLMVHGIGGASFNAGIKSYLVSGWSRGKLYAVDFWDKTGTNNYNGPQLASYVDRV 91
QY 62 LDETGAKKVDIVAHSMGGANTLYIKYKLDGKNVENVVTLGGTNRSTTSKALPGTDPNQK 121
Db 92 LKETGAKKVDIVAHSMGGANTLYIKYLGGNKIQNVTLGGANGLVSTALPGTDPNQK 151
QY 122 ILVTSYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
Db 152 ILVTSYSLNDQIVNSLSRQAGNIQLYGIGHIGLLNSQVNGYIKKEGLNGGLNTN 210
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RX MEDLINE=22617435; PubMed=12732514;
RA Akutsu-Shigeno Y., Teeraphatpornchai T., Teamtisong K., Nomura N.,
RA Uchiyama H., Nakahara T., Nakajima-Kambe T.;
RT "Cloning and Sequencing of a Poly(DL-Lactic Acid) Depolymerase Gene
RT from Paenibacillus amylolyticus Strain TB-13 and Its Functional
RT Expression in Escherichia coli.";
RL Appl. Environ. Microbiol. 69:2498-2504 (2003).
DR EMBL: AB093482; BAC67195.1; -.
DR GO: GO:0003824; F:catalytic activity; IEA.
DR GO: GO:0016298; F:lipase activity; IEA.
DR GO: GO:0016042; F:lipid catabolism; IEA.
DR InterPro: IPR002918; Lipase_2.
DR InterPro: IPR000379; Ser_estrs.
DR Pfam: PF01674; Lipase_2; 1.
SQ SEQUENCE 201 AA; 21661 MW; 4771183D38B7FBE1 CRC64;

Query Match 45.9%; Score 431; DB 2; Length 201;
Best Local Similarity 52.9%; Pred. No. 2.5e-26;
Matches 91; Conservative 24; Mismatches 51; Indels 6; Gaps 1;

QY 1 EHNPMVVMVHGIGGASFNAGIKSYLVSGWSRGKLYAVDFWDKTGTNNYNGPVLRSFVKK 60
Db 34 ERTTIVFVHGLTGTSDSNFALIERYLGRGESSDELFADLPFKAGNQLLNAAALSRFVDD 93
QY 61 VLDETGAKKVDIVAHSMGGANTLYIKYKLDGKNVENVVTLGGTNRSTTSKALPGTDPNQ 120
Db 94 VLRTGSKVHIVAHSMGGANSLYILNRGGIDKVDKLTILGGANRLTTSRDPG----- 148
QY 121 KILVTSYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGL 172
Db 149 -IRVTSYSTSTIVSPALSRDGNANISVNLVTHIGLLYNSRYNALIKAAAL 199

RESULT 6
Q826T6 PRELIMINARY; PRT; 228 AA.
AC Q826T6;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Putative lipase.
GN SAV7089.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531 (2003).
DR EMBL: AF050549; BAC74800.1; -.
DR GO: GO:0003824; F:catalytic activity; IEA.
DR GO: GO:0016298; F:lipase activity; IEA.
DR GO: GO:0016042; F:lipid catabolism; IEA.
DR InterPro: IPR002918; Lipase_2.
DR InterPro: IPR000379; Ser_estrs.
DR Pfam: PF01674; Lipase_2; 1.
```

KW Complete proteome. 228 AA; 24450 MW; C736C01EFF0F9DA9 CRC64;
SQ SEQUENCE 228 AA; 24450 MW; C736C01EFF0F9DA9 CRC64;

Query Match 21.5%; Score 202; DB 16; Length 228;
Best Local Similarity 29.1%; Pred. No. 3.6e-08;
Matches 52; Conservative 33; Mismatches 66; Indels 28; Gaps 4;

QY 2 HNPVVMHVGIGGASFNAGIKSVYLSQWGRGKLYAVDFW--DKTGTNNYNGPVLGRFVK 59
DB 35 HDPVIFVHGIGSSASSWDDMTADFEADGYTASEL---DAMSYDWSQSNVTTAQQLATEVR 91
QY 60 KVLDEGAKVDIVVAHSGGANTLYIKNLGGKNKVENVTGLGTNRETT----- 109
DB 92 SVLARTGASKVDLVVHSGMALSARYLKNLGGTGYDVFSTAGVNRHGTTVASCKWLYT 151
QY 110 -----SKALPCTDNQKILYTSIYSSA-DMIVMNYLSKLDGAKNVOIHGVGH 155
DB 152 SCSEMYTGSSFLTSLSNGDETPGGVAVASYNSCNDLLTPTDSAILSGATNVEGCVSH 210

RESULT 7
Q828V2 PRELIMINARY; PRT; 286 AA.
AC Q828V2;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Putative secreted lipase.
GN SAV6559.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.,
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites."
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis."
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AF005047; BAC74270.1; -
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0016298; F: lipase activity; IEA.
DR GO; GO:0016042; P: lipid catabolism; IEA.
DR InterPro; IPR002918; Lipase 2.
DR InterPro; IPR000379; Ser. esters.
DR Pfam; PF01674; Lipase_2; 1.
KW Complete proteome.
SQ SEQUENCE 286 AA; 30158 MW; 29A8703DD3BF853 CRC64;

Query Match 20.6%; Score 193.5; DB 16; Length 286;
Best Local Similarity 35.1%; Pred. No. 2.3e-07;
Matches 54; Conservative 23; Mismatches 60; Indels 17; Gaps 5;

QY 4 PVMVHVG-IGGASFNAGIKSVYLSQW-----SRGKLYAVDFWKTGTNNYNGPVLGRF 57
DB 52 PVLVHGTGNSVDNWLGLAPYLEHGGYCVFSLDYGQLSGVFFHGLGPIDKASQQLQVF 111
QY 58 VKKVLDEGAKVDIVVAHSGGANTLYIKNLGGKNKVENVTGLGTNRSTSKAL----- 113

DB 112 VDKVLTATGATKADLVHSGQGMPPRYLYKLGAGKKNALVGIAPNNHGTTLGLTLL 171
QY 114 ---PCTDENQKILYTSIYSSADMIYMN-YLSKLD 143
DB 172 PVFPGA---EDLSTATPGLADQVVGSAFMAKLN 202

RESULT 8
Q9RSP6 PRELIMINARY; PRT; 237 AA.
AC Q9RSP6;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Lipase, putative.
GN DR2078.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eissen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Koffat K.S., Qin H., Jiang L., Panchile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Uitterback T., Zaleski C.,
RA Makareva K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1."
RL Science 286:1571-1577(1999).
DR EMBL; AE003044; AAF11628.1; -
DR PIR; G75316; G75316.
DR TIGR; DR2078; -
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0016298; F: lipase activity; IEA.
DR GO; GO:0016042; P: lipid catabolism; IEA.
DR InterPro; IPR002918; Lipase 2.
DR InterPro; IPR000379; Ser. esters.
DR Pfam; PF01674; Lipase_2; 1.
KW Complete proteome.
SQ SEQUENCE 237 AA; 25308 MW; 1C2BF99210B8AF2E CRC64;

Query Match 20.6%; Score 193; DB 16; Length 237;
Best Local Similarity 29.1%; Pred. No. 1.9e-07;
Matches 55; Conservative 37; Mismatches 75; Indels 22; Gaps 5;

QY 3 NPVVMHVGIGGASFNAGIKSVYLSQWGRGKLYAVDFWKTGTNNYNGPVLGRFVKYL 62
DB 46 HPVLFVHGFNSDGSINWSPMNRFPKQDGTDAQLFSWSY--DSFKSNVATADLLRQKVDAIL 104
QY 63 DETGAKKVDIVVAHSGGANTLYIKNLGGKNKVENVTGLGTNR-----STTS---- 110
DB 105 AQTGAQVDIVHSGMALSARYLKNLGGTGYDVFSTAGVNRHGTTFALACSTACIEM 164
QY 111 -----KAL-PCTDENQKILYTSIYSSADMIY-MNYLSKLDGAKNVOIHGVGHGLL 161
DB 165 ROGSSFIKALNSGDETPGAVRYATWSPCDAVINPNSVPLSGATNTKTSCLTHSSLYGD 224
QY 162 SQVNSLIKE 170
DB 225 ATVTQVRD 233

RESULT 9
Q9KY65 PRELIMINARY; PRT; 331 AA.
ID Q9KY65
AC Q9KY65;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)

```
01-OCT-2003 (TRENBLrel. 25, Last annotation update)
Putative secreted lipase.
SC04799 OR SC63A.10C.
Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
[1]
SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Brown S.P., Harris D.;
RA Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cordero A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RA Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RA "A set of ordered cosmid and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
[4]
SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cordero-Narraga A.-M., Challis G.L.,
RA Thomson N.R., James K.B., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seger K., Saunders D., Sharp S., Squares R., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939121; CAB92662.1;
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004298; F:lipase activity; IEA.
DR GO; GO:0016042; F:lipid catabolism; IEA.
DR InterPro; IPR002918; Lipase 2.
DR InterPro; IPR008262; Lipase AS.
DR Pfam; PF01674; Lipase 2; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
DR Complete proteome.
KW SEQUENCE 331 AA; 35137 MW; 3E0E77A687747211 CRC64;
Query Match 19.2%; Score 180.5; DB 16; Length 331;
Best Local Similarity 26.7%; Pred. No. 2.9e-06;
Matches 54; Conservative 41; Mismatches 78; Indels 29; Gaps 6;
QY 4 PYVWHGIGGAGFNFAGIKSYLVSGWSRGKLYAVDFWDKGTGTYNNGPVLRFVKKVLD 63
DB 115 PVVLLHGFIDNRSVFLRLRSITQHG--RQIESLNSYPLTCDIRTAELLGRHIEICE 172
QY 64 ETGAKKVDIVAHSMGGANTLYIKNLGDKGNKVENVVTGGTNRSTTSKAL----- 113
DB 173 RTGSEVVDVGHSLGGLIARYVQRLGDLRVRTLTGLTGTGVPLANAHPIVRQM 232
QY 114 -PGT-----DPNQKILYTSIYSSADMIVNYSK--LD----GAKNVIHGVGHIG 157
DB 233 RPSGAVIEELTRPAPGCRTRFVSFNSDLDR--VNDPLETACLDHPDLSVQNVRSVGHILA 291
QY 158 LLMNSQVNSLIKEGLNGGLNT 179
DB 292 LPVHPAVATGIRQALDAGPET 313
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RESULT 10
Q82HP7 PRELIMINARY; PRT; 286 AA.
AC Q82HP7;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Putative lipase.
GN SAV3461.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horioka H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AF005035; BAC71173.1;
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR008262; Lipase AS.
DR InterPro; IPR000379; Ser esters.
DR PROSITE; PS00120; LIPASE_SER; 1.
DR Complete proteome.
KW SEQUENCE 286 AA; 30720 MW; 1C5CE9B2F12B2DD9 CRC64;
Query Match 18.4%; Score 172.5; DB 16; Length 286;
Best Local Similarity 25.2%; Pred. No. 1e-05;
Matches 51; Conservative 41; Mismatches 75; Indels 35; Gaps 5;
QY 4 PYVWHGIGGAGFNFAGIKSYLVSGWSRGKLYAVDFWDKGTGTYNNGPVLRFVKKVLD 63
DB 76 PVVLLHGFIDNRSVFLRLRSITQHG--RQIESLNSYPLTCDIRTAELLGRHIEICE 133
QY 64 ETGAKKVDIVAHSMGGANTLYIKNLGDKGNKVENVVTGGTNRSTTSKAL----- 113
DB 134 RTGSEVVDVGHSLGGLIARYVQRLGDLRVRTLTGLTGTGVPLANAHPIVRQM 193
QY 114 -PGT-----DPNQKILYTSIYSSADMIVNYSKLDGA-----KNVQIHGVG 154
DB 194 RPSGAVIEELTRPAPGCRTRFVSFNSDLDR--VNDPLETACVHPDLMVQNVRSVIG 249
QY 155 HIGLLMNSQVNSLIKEGLNGGG 176
DB 250 HLPVHPAVATGIRQALDSEG 271
RESULT 11
Q9S295 PRELIMINARY; PRT; 290 AA.
AC Q9S295;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Putative secreted lipase.
GN SC01735 OR SC111.24C.
```

OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Saunders D., Harris D.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
[3]
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8943436;
RA Redenbach M., Kieser H.M., Denapite D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
[4]
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=1200953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939110; CAB50950.1; -.
DR PIR; T36757; T36757.
DR HSP; Q05489; ITH.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0016298; F: lipase activity; IEA.
DR GO; GO:0016042; F: lipid catabolism; IEA.
DR InterPro; IPR002918; Lipase 2.
DR InterPro; IPR000379; Sex. esters.
DR Pfam; PF01674; Lipase_2; 1.
KW Complete proteome.
SQ SEQUENCE 290 AA; 30496 MW; D5GE8508350F7432 CRC64;

Query Match 18.1%; Score 170; DB 16; Length 290;
Best Local Similarity 29.2%; Pred. No. 1.7e-05;
Matches 56; Conservative 28; Mismatches 58; Indels 50; Gaps 8;

QY 4 PVMVHGIGGASF-NFAGIKSVLSQGRKLYAVDFDKTGNTN--YNGPV-----L 54
DB 56 PVLVHGTFGNSVDNWLGLAPYLKNGKGYC---VFLSDYGLQPLGVPLFGLGPFVKSABQL 112
QY 55 SRFVKKVLDGTGAKKVDIVAHSMGGANTLYIKNLDGGKNVENVYTLGGTNRSTT-----S 110
DB 113 AAHVQKVLATGATGTEFLVGHSGGMPRYLKLFGAAEVNVALVGIAPSNHGTLSGLT 172
QY 111 KALP-----GTPDNQKILYTSYSSADMVWNYL 139
DB 173 RLFLPYFGAEDLLNEHTPALADQVGSVDLTFLNAGGDTVPGVRYTVLTKYDEVVTYR 232
QY 140 SK-LD--GAKNV 148
DB 233 GQFLDGGFGRNV 244

RESULT 12

Q8RC83
ID Q8RC83 PRELIMINARY; PRT; 403 AA.
AC Q8RC83;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Predicted acetyltransferases and hydrolases with the alpha/beta
DE Hydrolase fold.
GN LIPA OR TTE0555.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NB4 / JCM 11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AB013025; AM23831.1; -.
DR GO; GO:0016787; F: hydrolase activity; IEA.
DR GO; GO:0016298; F: lipase activity; IEA.
DR GO; GO:0016740; F: transferase activity; IEA.
DR GO; GO:0016042; F: lipid catabolism; IEA.
DR InterPro; IPR002918; Lipase 2.
DR InterPro; IPR000379; Sex. esters.
DR Pfam; PF01674; Lipase_2; 1.
KW Transferase; Hydrolase; Complete proteome.
SQ SEQUENCE 403 AA; 45221 MW; DC31D5E86EC2CAC4 CRC64;

Query Match 17.9%; Score 168; DB 16; Length 403;
Best Local Similarity 35.9%; Pred. No. 3.7e-05;
Matches 42; Conservative 16; Mismatches 41; Indels 18; Gaps 3;

QY 4 PVMVHGIGGASF-NFA-----GIKSVLSQGRKLYAVDFDKTGNTNNGPVYL 54
DB 102 PVLVHGSGSDANFFADPKRDGSIITGLMQYLSQRGY---KVFATFAPHGDNVYIQREL 158
QY 55 SRFVKKVLDGTGAKKVDIVAHSMGGANTLYIKN-----LDGGKNVENVYTLGGTN 105
DB 159 ADVIQKVKATGASKVDIVAHSGKNMSARMYVSNVKSWSGVDFGKDVREYIQLGAPN 215

RESULT 13
P73372
ID P73372 PRELIMINARY; PRT; 202 AA.
AC P73372;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (PMGA).
GN SLL1969.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugiyura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Natuo K., Okumura S.,
RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
RN [2]
RP SEQUENCE OF 27-202 FROM N.A.
RA Hinara Y., Ikeuchi M.;

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OM protein - protein search, using sw model

Run on: April 23, 2004, 10:01:57 ; Search time 9.18367 Seconds
(without alignments)
1020.575 Million cell updates/sec

Title: US-09-905-666A-75

Perfect score: 939
Sequence: 1 EHNPFVVMVHGIGGASFNFA.....NSQVNSLIKEGLNGGLNTN 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	884	94.1	212	1 LIP_BACSU	P37957 bacillus su
2	129.5	13.8	358	1 LIP_PSEGL	O05489 pseudomonas
3	118.5	12.6	364	1 LIP_BURGE	P22088 burkholderi
4	118.5	12.6	364	1 LIP_PSEBS	P25275 pseudomonas
5	114	12.1	312	1 LIP_VIBCH	P15493 vibrio chol
6	103	11.0	737	1 ALYS_ENTFA	P37710 enterococcu
7	96.5	10.3	681	1 LIP_STAEP	Q99XQ0 staphylococ
8	95.5	10.2	688	1 LIP_STAEP	O02510 staphylococ
9	94.5	10.1	293	1 WHEP1_ECCLI	P77044 escherichia
10	90	9.6	562	1 WHEP1_ECCHA	P46508 schistosoma
11	89.5	9.5	690	1 LIP_STAAR	P10335 staphylococ
12	89.5	9.5	690	1 LIP_STAAR	Q8NYC2 staphylococ
13	88	9.4	431	1 ENO_SHEON	Q8EBR0 shewanella
14	86	9.2	277	1 BPHD_PSES1	P17548 pseudomonas
15	86	9.2	1052	1 RT32_ACTPL	P55131 actinobacil
16	85.5	9.1	605	1 AOR_PYRPU	O51739 pyrococcus
17	85	9.1	326	1 TGL2_YEAST	P54857 saccharomyc
18	84.5	9.0	351	1 ADH_CLORE	P25984 clostridium
19	84	8.9	268	1 ESL2_MYCPN	P75311 mycoplasma
20	83.5	8.9	373	1 ACCC_ALCEU	P27747 actinigenes
21	83.5	8.9	1113	1 MGA2_YEAST	P40578 saccharomyc
22	82.5	8.8	234	1 PUR7_STRA3	Q8E7X2 streptococc
23	81.5	8.7	277	1 LIP_PSEFR	P08658 pseudomonas
24	81	8.6	1754	1 WPEE_CHLTR	O64418 chlamydia t
25	80.5	8.6	415	1 YEGM_ECCLI	P76397 escherichia
26	80.5	8.6	607	1 AOR_PYRAB	O9V035 pyrococcus
27	80	8.5	313	1 YKLJ_YEAST	P28321 saccharomyc
28	79.5	8.5	236	1 PUR7_LACIA	O68830 lactococcus
29	79.5	8.5	245	1 FEGF_CAUCR	Q06171 caulobacter
30	79.5	8.5	286	1 BPHD_BURCE	P47229 burkholderi
31	79.5	8.5	288	1 Y134_MYCTU	O50599 mycobacteri
32	79.5	8.5	306	1 MIAA_BORBU	O51761 borrelia bu
33	79.5	8.5	331	1 KEAK_DROME	O18391 drosophila

ALIGNMENTS

RESULT 1

LIP_BACSU
ID LIP_BACSU STANDARD; PRT; 212 AA.
AC P37957; Q34644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lipase precursor (SC 3.1.1.3) (Triacylglycerol lipase).
GN LIPB OR LIP OR BSU02700.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=92329538; PubMed=1320940;
RA Datois V., Baulard A., Schanck K., Colson C.;
RT "Cloning, nucleotide sequence and expression in Escherichia coli of a
RT lipase gene from Bacillus subtilis 168."
RL Biochim. Biophys. Acta 1131:253-260(1992).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97419516; PubMed=9274031;
RA Kumano M., Tamakoshi A., Yamane K.;
RT "A 32 kb nucleotide sequence from the region of the lincomycin-
RT resistance gene (22 degrees-25 degrees) of the Bacillus subtilis
RT chromosome and identification of the site of the lin-2 mutation."
RL Microbiology 143:2775-2782(1997).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Solotkin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaeser P., Goffeau A., Golligly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haeche J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Kaeremans D., Kasahara Y., Klaer-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidis A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mavel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro E., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivalta C., Roche E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeder R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,

34 79.5 8.5 514 1 TUBE_DROVI
35 79 8.4 362 1 MURC_SHEON
36 79 8.4 381 1 SUBN_BACNA
37 79 8.4 431 1 ENO_SALTY
38 79 8.4 485 1 Y045_MYCPN
39 78.5 8.4 326 1 VS09_ROTPT
40 78.5 8.4 369 1 MRP_ECCLI
41 78.5 8.4 607 1 AOR_PVRHO
42 78.5 8.4 691 1 COMA_NEIGO
43 78.5 8.4 1286 1 AIDA_ECCLI
44 78 8.3 719 1 CLIP_BACTK
45 77.5 8.3 311 1 LIP_PSEAE

Q08171 drosophila
Q8CX35 shewanella
P35835 bacillus su
Q8XGP6 salmonella
P75056 mycoplasma
P17466 porcine rot
P21590 escherichia
O58778 pyrococcus
P51973 neisseria g
Q03155 escherichia
Q45752 bacillus th
P26876 pseudomonas

Verrips C.T.;
"Cloning of the Pseudomonas glumae lipase gene and determination of
the active site residues.";
Appl. Environ. Microbiol. 58:3787-3791(1992).
[2]
SEQUENCE OF 40-54, AND CHARACTERIZATION.
RN
RP SPECIES=C.viscosum;
RC MEDLINE=95306500; PubMed=7786905;
RX
RA Taipa M.A., Liebston K., Costa J.V., Cabral J.M.S., Jaeger K.-E.;
RN "Lipase from Chromobacterium viscosum: biochemical characterization
indicating homology to the lipase from Pseudomonas glumae";
RL Biochim. Biophys. Acta 1256:396-402(1995).
[3]
RN X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RP SPECIES=P. glumae;
RC MEDLINE=94096522; PubMed=8405390;
RX
RA Noble M.E.M., Cleasby A., Johnson L.N., Emond M.R., Frenken L.G.J.;
RN "The crystal structure of triacylglycerol lipase from Pseudomonas
glumae reveals a partially redundant catalytic aspartate.";
RL FEBS Lett. 331:123-128(1993).
[4]
RN X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RP SPECIES=C.viscosum; STRAIN=ATCC 6918;
RX MEDLINE=96275556; PubMed=8683577;
RA Lang D., Hofmann B., Haalck L., Hecht H.-J., Spener F., Schmid R.D.,
RN Schomberg D.;
RA "Crystal structure of a bacterial lipase from Chromobacterium
viscosum ATCC 6918 refined at 1.6-A resolution.";
RL J. Mol. Biol. 259:704-717(1996).
CC -|- FUNCTION: HYDROLYSIS OF TRIGLYCERIDES.
CC -|- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -|- COFACTOR: Requires calcium.
CC -|- SUBUNIT: Monomer.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS
CC LIPASE FAMILY.

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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL: X70354; CAA49812.1; -
CC EMBL: A16323; CAA01279.1; -
CC EMBL: A32021; CAA02073.1; -
CC PIR: A48952; A48952.
CC PDB: 1TAH; 31-MAY-94.
CC PDB: 1CVL; 01-APR-97.
CC PDB: 1QGE; 06-MAY-99.
CC InterPro: IPR000073; A/b hydrolase.
CC InterPro: IPR008262; Lipase AS.
CC InterPro: IPR000379; Ser esters.
CC Pfam: PF00561; abhydrolase_1.
CC PROSITE: PS00120; LIPASE_SER; 1.
CC Hydrolase; Lipid degradation; Signal; Calcium; 3D-structure.
KW FT SIGNAL 1 39
FT CHAIN 40 358
FT ACT_SITE 126 126
FT ACT_SITE 302 302
FT ACT_SITE 324 324
FT DISULFID 229 308
FT MUTAGEN 54 54
FT MUTAGEN 126 126
FT MUTAGEN 160 160
FT MUTAGEN 180 180
FT MUTAGEN 280 280
FT MUTAGEN 280 280
FT MUTAGEN 302 302
FT MUTAGEN 302 302
FT CHAIN 40 358
FT ACT_SITE 126 126
FT ACT_SITE 302 302
FT ACT_SITE 324 324
FT DISULFID 229 308
FT MUTAGEN 54 54
FT MUTAGEN 126 126
FT MUTAGEN 160 160
FT MUTAGEN 180 180
FT MUTAGEN 280 280
FT MUTAGEN 280 280
FT MUTAGEN 302 302
FT MUTAGEN 302 302
H->A: NO LOSS OF ACTIVITY.
S->A: COMPLETE LOSS OF ACTIVITY.
D->E: NO LOSS OF ACTIVITY.
D->A: NO LOSS OF ACTIVITY.
D->E: NO LOSS OF ACTIVITY.
D->A: COMPLETE LOSS OF ACTIVITY.
D->E: NO LOSS OF ACTIVITY.
D->A: 75% LOSS OF ACTIVITY.

H->A: COMPLETE LOSS OF ACTIVITY.
A -> W (IN REF. 2).

FT	MUTAGEN	324	324
FT	CONFLICT	40	40
FT	TURN	43	44
FT	STRAND	50	53
FT	TURN	61	62
FT	HELIX	65	67
FT	TURN	70	71
FT	HELIX	72	78
FT	TURN	79	80
FT	STRAND	83	86
FT	TURN	89	90
FT	TURN	97	98
FT	HELIX	100	115
FT	TURN	116	116
FT	STRAND	120	125
FT	TURN	126	126
FT	HELIX	127	138
FT	TURN	140	142
FT	STRAND	143	149
FT	TURN	153	154
FT	HELIX	157	168
FT	TURN	170	171
FT	STRAND	173	174
FT	TURN	176	188
FT	HELIX	191	193
FT	TURN	196	204
FT	STRAND	205	206
FT	TURN	208	217
FT	HELIX	221	222
FT	TURN	223	223
FT	STRAND	226	228
FT	TURN	231	231
FT	STRAND	235	238
FT	TURN	239	240
FT	STRAND	241	248
FT	TURN	250	250
FT	STRAND	253	259
FT	TURN	260	261
FT	STRAND	262	267
FT	TURN	275	275
FT	HELIX	276	279
FT	TURN	281	284
FT	STRAND	295	297
FT	TURN	301	301
FT	STRAND	306	306
FT	TURN	307	310
FT	STRAND	314	315
FT	TURN	320	320
FT	STRAND	324	325
FT	TURN	326	328
FT	STRAND	329	333
FT	TURN	337	338
FT	HELIX	342	356
FT	TURN	357	358
SQ	SEQUENCE	358 AA; FE7B5D7A22EC6B4B CRC64;	
Query Match 13.8%; Score 129.5; DB 1; Length 358;			
Best Local Similarity 34.8%; Pred. No. 0.00081;			
Matches 40; Conservative 16; Mismatches 42; Indels 17; Gaps 6;			
QY	4	PYVYVHGIGGASFNRA-----GIKSYLVSGWSRGLKYAVD---FWDKGTGTNNNGPV 53	
Db	49	PVLVHGLAGTD-KFANVVDYVYWGIGSDLOSHG---AKYVYANVLSGFQSDGPN-GRGEQ 103	
QY	54	LSRFVKVLDGTGAKVDIVAHSMGGMANTLYIKNLDGNGKVENVTTLGGTNRST 108	
Db	104	LLAYVVKVLAATGATKVNLIHSGSGLTSRYA--AVAPQLVASVTITGTPHRGS 156	
RESULT 3			
LIP_BURCE	STANDARD; PRT; 364 AA.		
AC	P22088;		

DT	01-AUG-1991 (Rel. 19, Created)
DT	01-FEB-1996 (Rel. 33, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
GN	LIPA.
OS	Burkholderia cepacia (Pseudomonas cepacia).
OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC	Burkholderiaceae; Burkholderia.
OX	NCBI_taxid=292;
RN	[1]
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 45-66.
RC	STRAIN=DSM 3959;
RX	MEDLINE=91100343; PubMed=1987151;
RA	Jorgensen S., Skov K.W., Diderichsen B.;
RT	"Cloning, sequence, and expression of a lipase gene from Pseudomonas
RT	cepacia: lipase production in heterologous hosts requires two
RT	Pseudomonas Genes.";
RL	J. Bacteriol. 173:559-567(1991).
RN	[2]
RP	X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX	MEDLINE=97184684; PubMed=9032073;
RA	Kim K.K., Song H.K., Shin D.H., Hwang K.Y., Suh S.W.;
RT	"The crystal structure of a triacylglycerol lipase from Pseudomonas
RT	cepacia reveals a highly open conformation in the absence of a bound
RT	inhibitor.";
RL	Structure 5:173-185(1997).
RN	[3]
RP	X-RAY CRYSTALLOGRAPHY.
RX	MEDLINE=97184685; PubMed=9032074;
RA	Schrag J.D., Li Y., Cygler M., Lang D., Burgdorf T., Hecht H.-J.,
RA	Schmid R., Schomburg D., Rydel T.J., Oliver J.D., Strickland L.C.,
RA	Dunaway C.M., Larson S.B., Day T.J., McPherson A.;
RT	"The open conformation of a Pseudomonas lipase.";
RL	Structure 5:187-202(1997).
CC	-1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC	fatty acid anion.
CC	-1- COPACTOR: Requires calcium.
CC	-1- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS
CC	LIPASE FAMILY.
CC	-----
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; M58494; AAA50466.1; .
DR	PDB; 1OIL; 15-MAY-97.
DR	PDB; 2LIP; 12-MAR-97.
DR	PDB; 3LIP; 16-JUN-97.
DR	PDB; 1HQD; 22-AUG-98.
DR	PDB; 4LIP; 19-AUG-98.
DR	InterPro; IPR000073; A/b hydrolase.
DR	InterPro; IPR008262; Lipase AS.
DR	InterPro; IPR000379; Ser esters.
DR	Pfam; PF00561; abhydrolase_1.
DR	PROSITE; PS00120; LIPASE_SER; 1.
KW	Hydrolase; lipid degradation; Signal; Calcium; 3D-structure.
FT	SIGNAL 1 44
FT	CHAIN 45 364
FT	ACT_SITE 131 131
FT	ACT_SITE 286 286
FT	ACT_SITE 330 330
FT	TURN 48 49
FT	STRAND 55 58
FT	TURN 61 62
FT	STRAND 66 67
FT	TURN 70 72
FT	STRAND 71 72
FT	TURN 75 75
FT	HELI

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FT TURN 84 85
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FT TURN 335 339
FT TURN 343 344
FT TURN 348 362
FT TURN 363 364
SQ SEQUENCE 364 AA; 37494 MW; E9CD2DBFB5565859 CRC64;

Query Match 12.6%; Score 118.5; DB 1; Length 364;
Best Local Similarity 29.9%; Pred. No. 0.0072;
Matches 35; Conservative 19; Mismatches 42; Indels 21; Gaps 6;

QY 4 PVMVHGIGGASFNPAKISYLVSGW-----SRGKLYAVD---FWDKTGTNYNG 51
Db 54 PIIIVHGLSGTD-KYAGVLEY-----WYGIQEDLQONGATVYVANLSGFSQSDGPN-GRG 106
QY 52 PVLSPFVKVLDGTGAKKVDIVAHSMGGANTLYIKNLDDGNKVENVVTLLGGTNRST 108
Db 107 EQLLAYVTVTLAATGATKVNLVGHSGQLSRYVA--AVAPDLVASVTITGTPHRGS 161

RESULT 4
LIP_PSES5
ID LIP_PSES5 STANDARD; PRT; 364 AA.
AC P25275;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
GN LIP.
OS Pseudomonas sp. (strain KWI-56).
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=311;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 45-47.

```

```

RX MEDLINE=92118328; PubMed=1368739;
RA Iizumi T., Nakamura K., Shimada Y., Sugihara A., Tomimaga Y.,
RA Fukase T.;
RT "Cloning, nucleotide sequencing, and expression in Escherichia coli
RT of a lipase and its activator genes from Pseudomonas sp. KWI-56.";
RL Agric. Biol. Chem. 55:2349-2357(1991).
CC -|- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -|- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS
CC LIPASE FAMILY.
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; D10069; BAA0960.1; -
CC EMBL; S77842; AAC60400.1; -
CC HSSP; P22088; 3LTP.
CC InterPro; IPR000073; A/b_hydrolase.
CC InterPro; IPR008262; Lipase_AS.
CC InterPro; IPR000379; Ser_estrs.
CC Pfam; PF00561; abhydrolase_1.
CC PROSITE; PS00120; LIPASE_SER; 1.
CC Hydrolase; Lipid degradation; Signal.
KW SIGNAL 1 44
FT CHAIN 45 364 LIPASE.
FT ACT_SITE 131 131 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 286 286 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 330 330 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 364 AA; 37511 MW; F346CB8B2E94E27D CRC64;

Query Match 12.6%; Score 118.5; DB 1; Length 364;
Best Local Similarity 29.9%; Pred. No. 0.0072;
Matches 35; Conservative 18; Mismatches 43; Indels 21; Gaps 6;

QY 4 PVMVHGIGGASFNPAKISYLVSGW-----SRGKLYAVD---FWDKTGTNYNG 51
Db 54 PIIIVHGLSGTD-KYAGVLEY-----WYGIQEDLQONGATVYVANLSGFSQSDGPN-GRG 106
QY 52 PVLSPFVKVLDGTGAKKVDIVAHSMGGANTLYIKNLDDGNKVENVVTLLGGTNRST 108
Db 107 EQLLAYVTVTLAATGATKVNLVGHSGQLSRYVA--AVAPDLVASVTITGTPHRGS 161

RESULT 5
LIP_VIBCH
ID LIP_VIBCH STANDARD; PRT; 312 AA.
AC P15493; O07349; Q9KMU7;
DT 01-APR-1990 (Rel. 14, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lactonizing lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
GN LIPA OR HLYC OR VCA0221.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor O17 / Serotype O1;
RX MEDLINE=90286918; PubMed=2162464;
RA Alm R.A., Manning P.A.;
RT "Characterization of the hlyB gene and its role in the production of
RT the El Tor haemolysin of Vibrio cholerae O1.";
RL Mol. Microbiol. 4:413-425(1990).
RN [2]
RP IDENTIFICATION, AND REVISIONS.
RC STRAIN=El Tor O17 / Serotype O1;
RN [1]
RP Manning P.A.;

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Best Local Similarity 23.3%; Pred. No. 0.34; Matches 48; Conservative 32; Mismatches 90; Indels 36; Gaps 7;
10 GIGGASNFAGIKS-XLVSGWGRGKL---YAVDFWDTGTNNYNGPVL-----SRPVKK- 60
416 GSGSNNQSGTNTYYTVKSGDTLNKIAAQYGVSVANLRSWNGISGDLIFVGQKLVKKG 475
61 VLDETGAKKVDIVAHSMGGANTLYIKULDGGNKV----- 95
476 ASGNTGSGNNGGNNQSGTNTYYTKSGDTLNKIAAQYGVSVANLRSWNGISGDLIFAG 535
96 ENVVTLGTTNRSTTSKALPGTDPNQKILYTSIYSSADMVIMNYLSKLDGAKNVQIHGVGH 155
536 QKIIVKGTSGTNGSGSNGGNNQSGTNT-YVTIKSGDTLNKISAQFGVSVANLQAWN 594
156 I-GLMNSQVNSLKEGLNGGLNTN 180
595 IGSGLIFAGQKIIIVKKGANGSGTNTN 620

RESULT 7
LIP STAMP
ID LIP STAMP STANDARD; PRT; 681 AA.
AC Q990X0;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lipase precursor (EC 3.1.1.3) (Glycerol ester hydrolase).
GN LIP OR GEH OR SAV2671 OR SA2463.
OS Staphylococcus aureus (strain M50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI_TaxID=158878, 158879;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=M50 / ATCC 700699, and N315;
RX MEDLINE=21311952; PubMed=1418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshino A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratsuki K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus".
RL Lancet 357:1225-1240 (2001).
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
family.

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EMBL; AF003366; BAB58833.1; --
EMBL; AF003138; BAB43769.1; --
PIR; G90075; G90075.
DR InterPro; IPR005877; Gpos_Y5IRK.
DR InterPro; IPR006262; Lipase_AS.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF04650; Y5IRK_signal; 1.
DR TIGRFAMs; TIGR01168; Y5IRK_signal; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation; Zymogen; Signal; Complete proteome.
FT SIGNAL 1 35
PROPSEP 36 291 BY SIMILARITY.

FT CHAIN 292 681 LIPASE.
FT ACT_SITE 409
FT ACT_SITE 640
FT ACT_SITE 640
SQ SEQUENCE 681 AA; 76662 MW; FE428D6F3B4B2CB4 CRC64;
Query Match 10.3%; Score 96.5; DB 1; Length 681;
Best Local Similarity 22.2%; Pred. No. 1.1;
Matches 46; Conservative 28; Mismatches 62; Indels 71; Gaps 10;
QY 3 NPVVMVHGIGGASNFAGIKSYLVSGWGRGKLXAVDFWDTGTNNYNGPVLRSFVKVL 62
Db 318 NPSVLAHYWGNGKN---IRQDLENGY---KAVEASI-SAFGSDYDRAVELYYVKGGR 370
QY 63 DETGA-----KKVDIVAHSMGGANTLYIKUL----- 89
Db 371 VDYGAHAAYCHERYGKTYEGYKDWKPKQKHLVGHSMGG-QTIQLELLNGHREE 429
QY 90 -----DGG-----NKNVNVTLGTTNRSTTSKALPGTDPNQKILYTSIYSSAD 132
Db 430 IEYQKHGGEISPLFKGNNNDNMISITLTGPHNGTHASDLAG---NEALVRQIVFD--- 483
QY 133 MIVMNYLSKLDGAKNVQI-HGVGHIGL 158
Db 484 -----IGKMFQKNKNSRVDFGLAQWGL 504

RESULT 8
LIP STAMP
ID LIP STAMP STANDARD; PRT; 688 AA.
AC Q02510;
DT 01-JUN-1994 (Rel. 29, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lipase precursor (EC 3.1.1.3) (Glycerol ester hydrolase).
GN LIP OR GEH OR SE0281.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI_TaxID=1282;
[1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 303-315.
RC STRAIN=9;
RX MEDLINE=93171870; PubMed=8436947;
RA Farrell A.M., Foster T.J., Holland K.T.;
RA "Molecular analysis and expression of the lipase of Staphylococcus
RT epidermidis".
RL J. Gen. Microbiol. 139:267-277 (1993).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RX PubMed=12950922;
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA Qian Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
RT "Genome-based analysis of virulence genes in a non-biofilm-forming
RT Staphylococcus epidermidis strain (ATCC 12228)".
RL Mol. Microbiol. 49:1577-1593 (2003).
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
family.

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EMBL; M95577; AAA19729.1; --
EMBL; AB016744; AAC03878.1; --
PIR; A47705; A47705.

DR InterPro; IPR005877; Gpos_Y5IRK.
DR InterPro; IPR008262; Lipase AS.
DR InterPro; IPR000379; Ser esters.
DR Pfam; PF04650; Y5IRK signal; 1.
DR TIGfam; TIGR01168; Y5IRK signal; 1.
DR PROSITE; PSC0120; LIPASE SER; 1.
KW Hydrolyase; Lipid degradation; Zymogen; Signal; Complete proteome.
FT SIGNAL 1 35
FT PROPEP 36 302
FT CHAIN 303 688
FT ACT SITE 418 648
FT ACT SITE 648 648
FT CONFLICT 96 96
FT CONFLICT 120 120
SQ SEQUENCE 688 AA; 77343 MW; 6C95D33A78AF86F6 CRC64;

Query Match 10.2%; Score 95.5; DB 1; Length 688;
Best Local Similarity 22.7%; Pred. No. 1.4;
Matches 47; Conservative 27; Mismatches 62; Indels 71; Gaps 9;

QY 3 NPVVMVHGIGGASFPAGFKSVLSQSGSRGKLYAVDFWDTGTNNNGPVLRSFVKVL 62
DB 327 NPSVLTHYGGDKM---IRQLENGEYAYEASISAP-----GSNYDRAVELYIYKGR 379
QY 63 DETGA-----KKVDIVAHSMGGANTLYIYKML----- 89
DB 380 VDYGAHAAYKGYKTYEGYKDWKPGQKIHVLVGHSMGG-QTIROLEELLRHGNEE 438
QY 90 -----DGG--NKVENVVTLLGGTNRSTTSKALPGTDPNPKILYTSYSSAD 132
DB 439 VEYQKHGEISPLYGQGHNDNMVSSITLTGTPHNGTHASDLLG---NEAIVRLAYD--- 492

QY 133 MIWNYLSKLDGAKVQI-HGVGHIGL 158
DB 493 -----VGRMYGNKDSRVDFGLEHWGL 513

RA Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K.,
RA Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -!- PATHWAY: 3-hydroxyphenylpropionate degradation.
CC -!- SIMILARITY: STRONG, TO B.CEPACIA AND PSEUDOMONAS BPMD.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; D86239; BAA13054.1; -
DR EMBL; Y05555; CAA70749.1; -
DR EMBL; A000142; AAC73452.1; ALT_INIT.
DR EMBL; U73557; AAB18073.1; ALT_INIT.
DR MEROPS; S33-UNW; -
DR EcoGene; EG20275; mhpc.
DR InterPro; IPR000073; A/b hydrolase.
DR InterPro; IPR003089; AB hydrolase.
DR InterPro; IPR000639; Epox hydrolase.
DR InterPro; IPR000379; Ser esters.
DR Pfam; PF00561; abhydrolase; 1.
DR PRINTS; PR00111; ABHYDROLASE.
DR PRINTS; PR00412; EPOXYDEHLASE.
KW Automatic hydrocarbons catabolism; Hydrolase; Complete proteome.
FT ACT SITE 90 90 BY SIMILARITY.
FT CONFLICT 158 158 E -> G (IN REF. 1 AND 2).
SQ SEQUENCE 293 AA; 32585 MW; 4407DF7B90EA0880 CRC64;

Query Match 10.1%; Score 94.5; DB 1; Length 293;
Best Local Similarity 25.1%; Pred. No. 0.61;
Matches 43; Conservative 36; Mismatches 61; Indels 31; Gaps 9;

QY 5 VVMVHGIG-GAS--FNPAGIKSVLSQSGSRGKLYAVDFWDTGTNNNG---PVLRSFV 58
DB 43 VLLHSGPGATGWANFSRNDIPLEAGY-RVLLDCPGHGKSDSVVSSRDLNARIL 101
QY 59 KKVLDETGAKKVDIVAHSMGGANTLYIYKLDGNGKVENVVTLL-GGTNRSTTSKALP--- 114
DB 102 KSVVDQLDIKIHLLGNSMGHSHVAF--TLKWPVRGKLVLMGGGTGMSLFTPMPTG 159
QY 115 -----GTPNQKILY-TSIYSSADMI-----VWNYLSKLDGAKN 147
DB 160 IKRLNQLYRQFTIENKLMMDIFVFTSDLTDLAFEARLNMLSRDHLN 210

RESULT 10
ID YME1_SCHWA STANDARD; PRT; 662 AA.
AC P46508;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE YME1 protein homolog (EC 3.4.24.-).
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Liberian;
RA Menath M.;
RL Thesis (1994), Heinrich-Heine University / Duesseldorf, Germany.
CC -!- FUNCTION: Putative ATP-dependent protease.
CC -!- COFACTOR: Binds 1 zinc ion (potential).
CC -!- SIMILARITY: Belongs to the AAA ATPase family.
CC -!- SIMILARITY: Belongs to peptidase family M41.
CC
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CC -----

CC EMBL; Z29947; CAAB2844.1; -
CC PIR; S42826; S42826.
CC MEROPS; M41.004; -
CC InterPro; IPR003593; AAA ATPase.
CC InterPro; IPR003959; AAA ATPase_cent.
CC InterPro; IPR003960; AAA sub.
CC InterPro; IPR005936; Peptidase_FtsH.
CC InterPro; IPR000642; Peptidase_M41.
CC Pfam; PF00004; AAA; 1.
CC Pfam; PF01434; Peptidase_M41; 1.
CC SMART; SMC0382; AAA; 1.
CC TIGRFAMs; TIGR01241; FtsH_fam; 1.
CC PROSITE; PS00674; AAA; 1.
CC ATP-binding; Hydrolase; Metalloprotease; Zinc.
CC NF_BIND 206 213 ATP (POTENTIAL).
CC ZINC (CATALYTIC) (BY SIMILARITY).
CC METAL 425 425 ZINC (CATALYTIC).
CC ACT_SITE 426 426 BY SIMILARITY.
CC METAL 429 429 ZINC (CATALYTIC) (BY SIMILARITY).
CC SEQUENCE 662 AA; 72939 MW; 8D36F28A9ACBBE75 CRC64;
CC -----

Query Match 9.6%; Score 90; DB 1; Length 662;
Best Local Similarity 26.5%; Pred.No. 3.9;
Matches 43; Conservative 22; Mismatches 73; Indels 24; Gaps 9;

QY 13 GASFNFAKISYLVQSWR-GKLYAVDFWMDKGTNYNGPVLRSRVKVLDTGAKVD 71
DB 232 GSSFD-----EVLVGLGASRIQLFT-----TAKQNSPCLV-FIDRI-DSVGNRTF 276
QY 72 IVAHSMGANTLYIKNLGDKGVNVTGGTNR--TTSKL--PGTDPNOKILVTSY 128
DB 277 SPHPFANQINQLLAEMDFQSGEGLVIGANQAEVLDKALLRQREDFDQIHVSPT 336
QY 129 SSADMIVMYLSKIDGAKVQI----HG-VGHIGLIMNSQVN 165
DB 337 EGRATLLNLYKKVKTGNSIDIEKLAHGTGVTGADIQNLVN 378

RESULT 11
LIP_STAAR
ID LIP_STAAR STANDARD; PRT; 690 AA.
AC P10335;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lipase precursor (EC 3.1.1.3) (Glycerol ester hydrolase).
GN LIP OR GER.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A. PubMed=3009394;
RX MEDLINE=86195821; PubMed=1548232;
RA Lee C.Y., Iandolo J.J.;
RT "Lysogenic conversion of staphylococcal lipase is caused by insertion
RT of the bacteriophage L54a genome into the lipase structural gene";
RL J. Bacteriol. 166:385-391 (1986).
RN [2]
RP PROCESSING, AND SEQUENCE OF 236-307.
RC STRAIN-TEN 5;
RX MEDLINE=92193269; PubMed=1548232;
RA Rollef J., Normark S.;
RT "In vivo processing of Staphylococcus aureus lipase";
RL J. Bacteriol. 174:1844-1847 (1992).
CC -!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -!- SUBCELLULAR LOCATION: Secreted.

-!- MISCELLANEOUS: The expression of Staphylococcus lipase is
negatively regulated by bacteriophage lysogenization (lipase
conversion).
-!- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
family.

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EMBL; M12715; AAA26633.1; -
PIR; A24545; A24545.
HSSP; P00192; 256B.
InterPro; IPR005877; Gpos_Ysirk.
InterPro; IPR008262; Lipase_AS.
InterPro; IPR000379; Ser_estrs.
Pfam; PF04650; Ysirk_signal; 1.
TIGRFAMs; TIGR01168; Ysirk_signal; 1.
PROSITE; PS00120; LIPASE_SER; 1.
Hydrolase; Lipid degradation; Zymogen; Signal.
SIGNAL 1 37 POTENTIAL.
PROPEP 38 295
CHAIN 296 690 LIPASE.
DOMAIN 311 690 HYDROPHOBIC.
ACT_SITE 412 412 CHARGE RELAY SYSTEM (BY SIMILARITY).
ACT_SITE 645 645 CHARGE RELAY SYSTEM (BY SIMILARITY).
SEQUENCE 690 AA; 76388 MW; 8E8E3654D0E01A3B CRC64;

Query Match 9.5%; Score 89.5; DB 1; Length 690;
Best Local Similarity 23.3%; Pred.No. 4.5;
Matches 47; Conservative 21; Mismatches 55; Indels 79; Gaps 8;

QY 4 PVMVHGI-----GGASFNFAKISYLVQSWRGLKLYAVDFWMDKGTN 47
DB 306 PVFVHGFLGLVGNAPALYNYWGNKFK---VIEELRQGVNVHQAQVSFAF---GSN 358
QY 48 YNNGPVLRSRVKVLDTGTA-----KVDIVAHSMGGANT 82
DB 359 YDRAVELYIYIKGRVDYGAHAAKYGHERYKTYKIMPNWEPKGLVHGHSMGGQTI 418
QY 83 LYIKNLGDKGVN-----NVVTLGGTNR-----STISKALP-----GTD 117
DB 419 RLMEFLNGKKEELAYHKAHGGISPLFTGCHNNMVASITTLATPHNGSQADKFGNTE 478
QY 118 PNQILYT-----SIYSSADM 133
DB 479 AVRKIMFALNRFMGNKYSNIDL 500

RESULT 12
LIP_STAAR
ID LIP_STAAR STANDARD; PRT; 690 AA.
AC Q8NYC2;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lipase precursor (EC 3.1.1.3) (Glycerol ester hydrolase).
GN LIP OR GER OR MW0297.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=195620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12043378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano K., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramoto K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA";

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RL Lancel 359;1819-1827(2002).
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
CC family.
CC
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CC
CC EMBL; AF004823; BAB94162.1; -
DR InterPro; IPR005877; Gops_YSIK.
DR InterPro; IPR008262; Lipase AS.
DR InterPro; IPR000379; Ser esters.
DR Pfam; PF04650; YSIK signal; 1.
DR TIGRFAMs; TIGR01168; YSIK signal; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation; Zymogen; Signal; Complete proteome.
FT SIGNAL 1 37
FT PROPEP 38 295
FT CHAIN 296 690
FT ACT_SITE 412 412
FT ACT_SITE 645 645
FT ACT_SITE 645 645
SQ SEQUENCE 690 AA; 76522 MW; 36FF5E0EBB434CCA CRC64;

Query Match 9.5%; Score 89.5; DB 1; Length 690;
Best Local Similarity 23.3%; Pred. No. 4.5;
Matches 47; Conservative 21; Mismatches 55; Indels 79; Gaps 8;

QY 4 PVMVHGI-----GGASENFAGIKSVLSQSGSRGKLYAVDFWDXGTGN 47
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
306 PVFVHGFLGLVGDNAPALYNYGNGKFK---VIEELKQGINVHQASVAF---GSN 358
QY 48 YNNGPVLRFVKVLDLDTGA-----KKVDIVAHSMGGANT 82
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
359 YDRAVELYVYIKGRVDYGAHAAPKAGHYERYKTYKIMNPWBPCKKVLVGHSMGGQTI 418
QY 83 LYVIRNLGGKNVE-----NVVTLGQTNR---STTSKALP-----GTD 117
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
419 RLMSEFLRNGNKEEYAKHAGGELSLPLFTGHNWVASITTLATPNHGQAADKFGNTE 478

QY 118 PNQKILYT-----SIYSSADM 133
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
479 AVRKIMFALNRMGNKYSNIDL 500

RESULT 13
ENO SHEON STANDARD; PRT; 431 AA.
AC Q8EBR0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
DE Glycerate hydro-lyase).
GN ENO OR SO3440.
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OC NCBI_TaxID=70963;
RN [1] SEQUENCE FROM N.A.
RP STRAIN=NR-1;
RC MEDLINE=22597686; PubMed=12368813;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,

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RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA Vanathavan J., Weidman J., Imprim M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., C.M.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Neilson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis."
RL Nat. Biotechnol. 20:1118-1123(2002).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2)O.
CC -1- COFACTOR: Magnesium is required for catalysis and for stabilizing
CC the dimer (By similarity).
CC -1- PATHWAY: Glycolysis
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
CC
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CC
CC EMBL; AE015780; AAN56437.1; ALT_INIT.
DR TIGR; SO3440; -
DR HAMAP; MF_00318; -; 1.
DR InterPro; IPR000941; Enolase.
DR Pfam; PF00113; enolase; 1.
DR Pfam; PF03952; enolase N; 1.
DR PRINTS; PR00148; ENOLASE.
DR PRODOM; PD000902; Enolase; 1.
DR TIGRFAMs; TIGR01060; eno; 1.
DR PROSITE; PS00164; ENOLASE; 1.
KW Lyase; Glycolysis; Magnesium; Complete proteome.
FT ACT_SITE 159 159
FT ACT_SITE 246 246
FT METAL 289 289
FT METAL 316 316
FT METAL 316 316
SQ SEQUENCE 431 AA; 45686 MW; 3D7F1A0658328B12 CRC64;

Query Match 9.4%; Score 88; DB 1; Length 431;
Best Local Similarity 22.7%; Pred. No. 3.4;
Matches 47; Conservative 34; Mismatches 78; Indels 48; Gaps 10;

QY 3 NPVV--MVHGIGGASNFAGIKSVLSQSGSRGKLYAVDFWDXGTGN-----N 49
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
18 NPTVEAEVHLEGG---FIGMAA--APSGASTGSRLELRDGDGKRYLKGKGLTAVANV 71
QY 50 NGPVLRFVKVLDLDTGAKKVDIVAHSMGGANTLYYIKNLDDGKNVENVVTGGTNRSTT 109
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
72 NGPIRTALIGK--DATAQAELDQIMIDLDTGTE-----KDKLGANAI-LAVSLAAKAAAA 124
QY 110 SKALP-----GTD-----PNOKILYTSYSSADMVNNVYLSKLGAKNQVHG 153
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
125 FKMFLYAHIAELNGTGPQYAVPMPMNNILNGGHDANNVDIOEFMVQPVGAKNFR---- 180
QY 154 GHIGLLANNSOVNSLTKELNGGGGLNTN 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 --EALRMGAELFHTLKKVLHGKGLSIS 205

RESULT 14
BPHD_PSES1
ID BPHD_PSES1 STANDARD; PRT; 277 AA.
AC P17548;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase (EC 3.7.1.-).
GN BPHD.
OS Pseudomonas sp. (strain KKS102).
OC Bacteria; Proteobacteria.

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OX NCBI_TaxID=307;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=89213985; PubMed=2540155;
RA Kimbara K., Hashimoto T., Fukuda M., Koana T., Takagi M., Oishi M.,
RA Yano K.;
RT "Cloning and sequencing of two tandem genes involved in degradation
RT of 2,3-dihydroxybiphenyl to benzoic acid in the polychlorinated
RT biphenyl-degrading soil bacterium Pseudomonas sp. strain KKS102.";
RL J. Bacteriol. 171:2740-2747(1989).
CC
CC -!- PATHWAY: Degradation of biphenyls and polychlorobiphenyls (PCB) to
CC benzoic acid and chlorobenzoic acids.
CC -!- SIMILARITY: STRONG, TO E.COLI MHP.
CC
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CC
CC EMBL; M26433; AAA25751.1; -
CC PIR; B32312; ESPSK.
CC InterPro; IPR000073; A/b_hydrolase.
CC InterPro; IPR003085; AB_hydrolase.
CC InterPro; IPR000379; Ser_estrfs.
CC Pfam; PF00561; abhydrolase; 1.
CC PRINTS; PR00111; ABHYDROLASE.
CC Aromatic hydrocarbons catabolism; Hydrolase.
CC ACT_SITE 112 BY SIMILARITY.
CC ACT_SITE 112
CC SEQUENCE 277 AA; 30253 MW; E0C7496186818D1E CRC64;
CC
Query Match 9.2%; Score 86; DB 1; Length 277;
Best Local Similarity 27.1%; Pred. No. 3;
Matches 42; Conservative 21; Mismatches 44; Indels 48; Gaps 9;
QY 5 VVMVHGIGGASFNFAGIKSVLVSQWSR-----GKL-----YAVDFWPKTGTNNYNN----- 50
DB 36 VIMLHG-GGPG--AG-----GWSNYRNIGPFVEAGYRVLLPDAPGFNSDVTWMD 83
QY 51 ---GPVLRSFRVKVLDGTGAKKVDIVAHSMGGANTLYIYKNDGGNKVENVTLGTNRS 107
DB 84 EQRLGVNARSVKGMVDVLGIEKAHLVNSMGGAGALNFA--LEYPERTGKLILMG----- 136
QY 108 TTSKALPGTDNQKILYTSIYSSADMIVMNLVSLK 142
DB 137 -----PGG-----LGNSLFTAMPMEGIKLLFKL 159
RESULT 15
RT32 ACTPL STANDARD; PRT; 1052 AA.
AC P55131;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RTX-III toxin determinant A from serotype 8 (APX-IIIa) (Cytolysin
DE IIIa) (CLY-IIIa).
GN APXIIIa OR CLYIIIa OR RTXa OR PTXa.
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=715;
RN
RP SEQUENCE FROM N.A.
RX STRAIN=405 / Serotype 8;
RX MEDLINE=95012630; PubMed=7927703;
RA Jansen R., Briare J., van Geel A.B.M., Kamp E.M., Gielkens A.L.J.,
RA Smits M.A.;
RT "Genetic map of the Actinobacillus pleuropneumoniae RTX-toxin (ApX)
RT operons: characterization of the ApXIII operons.";
RL Infect. Immun. 62:4411-4418(1994).

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[2]
RN
RP SEQUENCE FROM N.A.
RX STRAIN=Serotype 8;
RX MEDLINE=93162836; PubMed=8432615;
RA Jansen R., Briare J., Kamp E.M., Gielkens A.L.J., Smits M.A.;
RA "Cloning and characterization of the Actinobacillus
RT pleuropneumoniae-RTX-toxin III (ApXIII) gene.";
RL Infect. Immun. 61:947-954(1993)
CC
CC -!- FUNCTION: Does not have hemolytic activity but shows a strong
CC cytotoxicity towards alveolar macrophages and neutrophils.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: The Gly-rich region is probably involved in binding
CC calcium, which is required for target cell-binding or cytolytic
CC activity (By similarity).
CC -!- DOMAIN: The three transmembrane domains are believed to be
CC involved in pore formation by the cytotoxin (By similarity).
CC -!- PTM: Palmitoylated by apXIIIc. The toxin only becomes active when
CC modified (By similarity).
CC -!- SIMILARITY: Belongs to the RTX prokaryotic toxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X80055; CAA56358.1; -
CC EMBL; X68815; CAA48711.1; -
CC PIR; B49219; B49219.
CC InterPro; IPR001343; Hemlysn_Ca_bind.
CC InterPro; IPR003995; RTXa.
CC Pfam; PF00353; hemolysinCbind; 6.
CC Pfam; PF02382; RTX; 1.
CC PRINTS; PR00313; CABDNGRPT.
CC PRINTS; PR01488; RTXTOXINA.
CC PROSITE; PS00330; HEMOLYSIN_CALCIUM; 3.
CC Toxin; Cytolysis; Repeat; Calcium; Transmembrane; Lipoprotein;
KW Palmitate.
FT TRANSMEM 248 265 POTENTIAL.
FT TRANSMEM 275 334 POTENTIAL.
FT TRANSMEM 372 418 POTENTIAL.
FT DOMAIN 754 859 7 X REPEATS, GLY-RICH.
FT REPEAT 754 759 1.
FT REPEAT 763 768 2.
FT REPEAT 772 777 3.
FT REPEAT 781 786 4.
FT REPEAT 790 795 5.
FT REPEAT 799 804 6.
FT REPEAT 808 813 7.
FT REPEAT 827 832 8.
FT REPEAT 836 841 9.
FT REPEAT 845 850 10.
FT REPEAT 854 859 11.
FT SEQUENCE 1052 AA; 112809 MW; F83AFE25A6FD8758 CRC64;
SQ
Query Match 9.2%; Score 86; DB 1; Length 1052;
Best Local Similarity 22.1%; Pred. No. 15;
Matches 33; Conservative 23; Mismatches 47; Indels 46; Gaps 7;
QY 41 WDKTGTNNNGFVLSRFVKVLDGTGAKKVDIVAHSMGGANTLYIYKNDGGNKVENVVT 100
DB 922 WFKEGKNYHK-----IEQIVDKNGRK--LTAENLG-----TYFKNAKPADNLLNAT 967
QY 101 LGGTRSTTSKALPGTDNQKILYTSIYSSADMIVMNLVSLKLDGKKNVQIHGVGHGL-- 158
DB 968 KEDQNESNLS-----SLKTELSKIITN-----AGNFGVAKQGTGINT 1005
QY 159 -LWNSQVNSLIKEG-----LNGGGLNT 179
DB 1006 AALNNEVNNKIISSANTFATSQLGSGSGMT 1034

```

us-09-905-666a-75.rsp

Mon Apr 26 08:04:04 2004

Search completed: April 23, 2004, 10:12:31
Job time : 10.1837 secs

QY 121 KILYTSIYSSADMVNNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
Db 153 KILYTSIYSSADMVNNYLSRLDGRNVQIHGVGHIGLLYSSQVNSLIKEGLNGGQNTN 212

RESULT 2
lipase lipB - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: C69652
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brulliet, S.; Bruchli, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gallier
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koester, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Toynoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, K.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: C69652
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-210 <GUN>
A:Cross-references: GB:Z99108; GB:AL009126; NID:G2633055; PIDN:CAB12664.1; PID:e1182825;
A:Experimental source: strain 168
C:Genetics:
A:Gene: lipB

Query Match 76.0%; Score 714; DB 2; Length 210;
Best Local Similarity 74.3%; Pred. No. 1.2e-51;
Matches 133; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

QY 2 HNPVVMHIGIGASPNFAGIKSYLVSCQWSRGKLYAVDFWMDTKTNNYNGPVLRFVKKV 61
Db 32 HNPVLMHIGIGASPNFAGIKSYLVSCQWSRGKLYAVDFWMDTKTNNYNGPVLRFVKKV 91

QY 62 LDETCAKVDIVAHSMGANTLYIKNLGDKGNKVENVTGTRTTSKALPCTDPOK 121
Db 92 LKETCAKVDIVAHSMGANTLYIKNLGDKGNKVENVTGTRTTSKALPCTDPOK 151

QY 122 ILYTSIYSSADMVNNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
Db 152 ILYTSIYSSADMVNNYLSRLDGRNVQIHGVGHIGLLYSSQVNSLIKEGLNGGQNTN 210

RESULT 3
G75316
probable lipase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: G75316
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-237 <WHI>
A:Cross-references: GB:AE002044; GB:AE000513; NID:G6459872; PIDN:AAF11628.1; PID:G645987
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR2078

A:Map position: 1

Query Match 20.6%; Score 193; DB 2; Length 237;
Best Local Similarity 29.1%; Pred. No. 1.1e-08;
Matches 55; Conservative 37; Mismatches 75; Indels 22; Gaps 5;

QY 3 NPVVMHIGIGASPNFAGIKSYLVSCQWSRGKLYAVDFWMDTKTNNYNGPVLRFVKKV 62
Db 46 HNPVLMHIGIGASPNFAGIKSYLVSCQWSRGKLYAVDFWMDTKTNNYNGPVLRFVKKV 104

QY 63 DETCAKVDIVAHSMGANTLYIKNLGDKGNKVENVTGTRTTSKALPCTDPOK 110
Db 105 AQTGAQVDIVAHSMGANTLYIKNLGDKGNKVENVTGTRTTSKALPCTDPOK 164

QY 111 -----KAL-PGTPDQKILYTSIYSSADMV-NVYLSKLDGAKNVQIHGVGHIGLLM 161
Db 165 RQGSFFIKALNSGDETEGAVEYATWNSPCDAVINPNSVPLSGATNTKTSCLTHSSLYGD 224

QY 162 SOVNSLIKE 170
Db 225 ATVTQVRD 233

RESULT 4
T36757
probable secreted lipase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
R:Saunders, D.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A:Reference number: Z21613
A:Accession: T36757
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-290 <SAU>
A:Cross-references: EMBL:AL096849; PIDN:CAB50950.1; GSPDB:GN00070; SCOEDB:SCI11.24C
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCI11.24C

Query Match 18.1%; Score 170; DB 2; Length 290;
Best Local Similarity 29.2%; Pred. No. 1.1e-06;
Matches 56; Conservative 28; Mismatches 58; Indels 50; Gaps 8;

QY 4 PVMVVMHIGIGASPNFAGIKSYLVSCQWSRGKLYAVDFWMDTKTNNYNGPVLRFVKKV 54
Db 56 PVMVLMHIGIGASPNFAGIKSYLVSCQWSRGKLYAVDFWMDTKTNNYNGPVLRFVKKV 112

QY 55 SRPVKVDDETCAKVDIVAHSMGANTLYIKNLGDKGNKVENVTGTRTTSKALPCTDPOK 110
Db 113 AARVDKVLAAATGATGATETDLVGHSGQGMNRYLYKFGGAEEVNALVGIAPSNHGTTLGLT 172

QY 111 KALP-----GTPDQKILYTSIYSSADMVNNY 139
Db 173 RLPLPFGAEDLLNEHTPALADQVVGSDVLTSLNAGDTPGVRYTLATKYDEVVTPYR 232

QY 140 SK-LD--GAKNV 148
Db 233 GQFLDGPGRNV 244

RESULT 5
S77556
hypothetical protein sll1969 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S77556
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shampo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

T26657
hypothetical protein Y38E10A.g - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T26657
R:Wallis, J.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z20252
A:Accession: T26657
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-286 <WIL>
A:Cross-references: EMBL:AL110484; PIDN:CAB54398.1; CESP:Y38E10A.g
A:Experimental source: clone Y38E10A
C:Genetics:
A:Gene: CESP:Y38E10A.g
A:Introns: 63/2; 221/2; 261/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C09E8.2

Query Match 14.2%; Score 133; DB 2; Length 286;
Best Local Similarity 25.4%; Pred. No. 0.0012;
Matches 49; Conservative 25; Mismatches 65; Indels 54; Gaps 7;

QY 4 PVVMVHGIGGASFNAGIKSVLSQSGSRGKLYAVDFWDKGTGTYNNGPVLSPFVKV-- 61
DB 66 PVILVHGTTNSAGTAPQAAYFRANGSSEETVYATTYDAGVTTATNTVMKLCYVQGI 125
QY 62 ---LDETGAKKVDIVAHSMGGANTLYYIKNLGGNKVENVVILG-----G 103
DB 126 MIIAVNATQKXNVIGSMSPAR---KAILGKCAENVQLGAPLTSIIETIYSVAG 182
QY 104 TNRST-----TSKALPG-----TDPNQKILYT-----SIYSSAD----- 132
DB 183 ANRGTSLCDILFAPLWPTNTKNGKSGDFLDIRSVAYEGQYIFSIYGPSDDXVGF 242
QY 133 MIVMYLSKLDGA 145
DB 243 NTVGRVSKIDGA 255

RESULT 10
T27932
hypothetical protein ZK617.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27932
R:White, S.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z20442
A:Accession: T27932
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-344 <WIL>
A:Cross-references: EMBL:Z73897; PIDN:CAA98062.1; GSPDB:GN00022; CESP:ZK617.2
A:Experimental source: clone ZK617
C:Genetics:
A:Gene: CESP:ZK617.2
A:Map position: 4
A:Introns: 62/2; 121/3; 288/2

Query Match 13.9%; Score 130.5; DB 2; Length 344;
Best Local Similarity 25.9%; Pred. No. 0.0024;
Matches 52; Conservative 27; Mismatches 71; Indels 51; Gaps 9;

QY 4 PVVMVHGIGGASFNAGIKSVLSQSGSRGKLYAVDFWDKGTGTYNNGPVLSPVLS----- 55
DB 65 PVFVHGLNAGSLWKIARDFTNANPQYLFATT-MKGTEPLNLNVAMSGCTHVQVR 123
QY 56 RFVKVLDGTGAKKVDIVAHSMGGANTLYYI---KNLGGN-----KYENVVTLGG 103
DB 124 RFETVLKYTGAKIDVIGSMSPARAKAILGGKVDNPNVALGPSLSHRVHTIYSVAG 183
QY 104 TNRSTTSKALP-----GTDPNQKIL-----YTSIY-----SSADMIVNYL- 139

Db 184 ANQSQLCALPFFDICNMKTKGLMCKSKFEDINWFKNTYEGSKAFNLAFTADVVV-GYMA 242
QY 140 -----SKLDGAKNVQIHGVGH 155
DB 243 CGKKASEFTGAHEWKVEGRNH 263

RESULT 11
A49952
triacylglycerol lipase (EC 3.1.1.3) precursor - Pseudomonas glumae
C:Species: Pseudomonas glumae
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49952; S36248; S37291
R:Freken, L.G.J.; Bos, J.W.; Visser, C.; Tomassen, J.; Verrips, C.T.
Appl. Environ. Microbiol. 58, 3787-3791, 1992
A:Title: Cloning of the Pseudomonas glumae lipase gene and determination of the active s
A:Reference number: A49952; MUID:93119130; PMID:1476423
A:Accession: A49952
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <PRE>
A:Cross-references: EMBL:X70354; NID:G49205; PIDN:CAA49812.1; PID:G49206
A:Experimental source: PGI
A:Note: sequence extracted from NCBI backbone (NCBIN:121572, NCBI:121573)
R:Freken, L.G.J.; Bos, J.W.; Visser, C.; Mueller, W.; Tomassen, J.; Verrips, C.T.
Mol. Microbiol. 9, 579-585, 1993
A:Title: An accessory gene, lipB, required for the production of active Pseudomonas glum
A:Reference number: S36248; MUID:94018652; PMID:8412704
A:Accession: S36248
A:Molecule type: DNA
A:Residues: 316-358 <FR2>
A:Cross-references: EMBL:X70354
C:Genetics:
A:Gene: lipA
C:Superfamily: Pseudomonas triacylglycerol lipase
C:Keywords: carboxylic ester hydrolase; extracellular protein

Query Match 13.8%; Score 129.5; DB 1; Length 358;
Best Local Similarity 34.8%; Pred. No. 0.0031;
Matches 40; Conservative 16; Mismatches 42; Indels 17; Gaps 6;

QY 4 PVVMVHGIGGASFNFA-----GIKSVLSQSGSRGKLYAVD---FWDKGTGTYNNGPV 53
DB 49 PVILVHGLAGTD-KPANVVDVYVYQISDLQSHG---AKYVANLSGFQDDGPN-GRGQ 103
QY 54 LSRFVKVLDGTGAKKVDIVAHSMGGANTLYYIKNLGGNKVENVVTLGGTNRST 108
DB 104 LLAYVQVLAATGATKVNLIHSGQGLTSRYVA--AVAPQVASVTITGTPHRGS 156

RESULT 12
A97027
hydrolase of alpha/beta superfamily, probable membrane associated lipase [imported] - Cl
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: A97027
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: A97027
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-479 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK79004.1; PID:GI5023939; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1028

Query Match 13.4%; Score 126; DB 2; Length 479;
Best Local Similarity 22.0%; Pred. No. 0.0086;

Matches 54; Conservative 38; Mismatches 65; Indels 88; Gaps 12;
QY 4 PVMVHGIGGAS---FNFAG-IKSVLSQGWRSGLKLY--AVDFWTKTGTNNNGPVLRSF 57
DB 223 PVLVHGVRDLKYNWGRPKELIRNG---ATIIYGNQEA---GTVEYNAQYMKK 276
QY 58 VRKVLDTGAKKVDIVAHSMGGANTLYIYIKNLDGKNKVENVVTLGTTNR----- 106
DB 277 ILQIIKETCEKWNIIAHSGGLGDSRYMSKLEMGKYVASLTWMSGPHRGCKFVDIACKI 336
QY 107 -----SITS-----KALPGTDPNGKILYT 125
DB 337 PDKIYRAVNFFDKYKILGDKNPNDFYASRFSYSSKFNVEKDVPG-----VYIQ 390
QY 126 SIYSSADMVWNY-----LSKL-----DGAKNQIHWGHI--GLLMNSQVNSLIKEGL 172
DB 391 SVATAKNIFSDYVWISIPYVLKLTSGENDGLVSDSAKWGHFKGVIRNR-----RSGI 445
QY 173 NGGGL 177
DB 446 SHGDI 450
RESULT 13
T33322
hypothetical protein C09E8.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jun-2000
C:Accession: T33322
R:Du, Z.; Graves, T.; Gibson, A.
submitted to the EMBL Data Library, July 1998
A:Description: The sequence of Caenorhabditis elegans cosmid C09E8.
A:Reference number: Z21322
A:Accession: T33322
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-292 <DUZ>
A:Cross-references: EMBL:AF077529; PIDN:AA26254.1; GSPDB:GN00020; CBSP:C09E8.2
A:Experimental source: strain Bristol N2; clone C09E8
C:Genetics:
A:Gene: CESP:C09E8.2
A:Map position: 2
A:Introns: 80/3; 123/2; 166/1; 200/2
C:Superfamily: Caenorhabditis elegans hypothetical protein C09E8.2
Query Match 12.9%; Score 121; DB 2; Length 292;
Best Local Similarity 25.4%; Pred. No. 0.012;
Matches 44; Conservative 25; Mismatches 58; Indels 46; Gaps 6;
QY 3 NPVMVHGIGGASFNAGIKSVLSQGWRSGLKLYAVDFWTKTGTNNNGPVLRSFVKVY- 61
DB 64 NPVLIVHGITNKASRFGGTVAIYLSKSKYKSEIYGTWGDGSRTPVGLVDMKCNVYKQIR 123
QY 62 -----LDETGAKKVDIVAHSMGGANTLYIYIKNLDGKNKVENVVTLG----- 102
DB 124 AMIIAVRQYTGQKVDVIGYSMGSPFLAR---KAILGGQCVDTREILGAPLTVDTELSVA 180
QY 103 GTNRSTTSKALP---GT-----DPNQKILYT-----SIYSSAD 132
DB 181 GANYGSVLCILFVPGVGTGCKNKGHLHCDSEFLQDINNQHRYEGSHVFSIFSTAD 233
RESULT 14
B69470
lipase homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Jun-2000
C:Accession: B69470
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: B69470
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-474 <KLE>
A:Cross-references: GB:AE000981; GB:AE000782; NID:g2689304; PIDN:AA889488.1; PID:g264878;
C:Superfamily: Archaeoglobus fulgidus probable lipase AF1763

Query Match 12.8%; Score 120.5; DB 2; Length 474;
Best Local Similarity 20.7%; Pred. No. 0.024;
Matches 48; Conservative 37; Mismatches 66; Indels 81; Gaps 9;
QY 1 EHNPMVVMHGIGGASFNAGIKSVLSQGWRSRKLKLYAVDF-----W-----D 42
DB 21 DFRDVFVHGLAGSAGQFESQGMRFAGYPAEYVKTFFEYDTISWALVWETDMLFSLGLS 80
QY 43 KTGTNNY-----GPVLSRFVKVKLDET-----GAKKVDIVAHSMGGA 80
DB 81 EFLNISIQIIDPETLTKILSKSERLIDETFSRLDRVIDEALAESGADKVDLVCHSNSTF 140
QY 81 NTLYYIKNL-DGKNKVENVVTLGTT-----NRSTTSKALPGTD-PNQKI 122
DB 141 FLVRYVNSSPERAAKVAHLILLDGVWGVDAPGEGTPTLAVFGN-----PKALPALGLPEEKV 196
QY 123 LYTSIYSSADMVWNYLSKLDGAKNQIHWGHI--GLLMNSQVNSLIKEGLNG 174
DB 197 VY-----NATNVYFNNTVHVLCTSPETFAVMFEFNG 229

RESULT 15
A39133
triacylglycerol lipase (EC 3.1.1.3) precursor - Pseudomonas cepacia
C:Species: Pseudomonas cepacia
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A39133
R:Jorgensen, S.; Skov, K.W.; Diderichsen, B.
J. Bacteriol. 173, 559-567, 1991
A:Title: Cloning, sequence, and expression of a lipase gene from Pseudomonas cepacia: 1;
A:Reference number: A39133; MUID:91100343; PMID:1987151
A:Accession: A39133
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <JOK>
A:Cross-references: GB:M58494
C:Superfamily: Pseudomonas triacylglycerol lipase
C:Keywords: carboxylic ester hydrolase

Query Match 12.7%; Score 119.5; DB 1; Length 364;
Best Local Similarity 29.9%; Pred. No. 0.021;
Matches 35; Conservative 19; Mismatches 42; Indels 21; Gaps 6;
QY 4 PVMVHGIGGASFNAGIKSVLSQGW-----SRKLYAVD---FWDKGTNNNG 51
DB 54 PIILVHGLSGTD-KYAGVLEY-----WYGIQEDLQONGATVYVANLSGFSQDDGPN-GRG 106
QY 52 PVLRSFVKVKLDETGAKKVDIVAHSMGGANTLYIYIKNLDGKNKVENVVTLGTTNRST 108
DB 107 EQLLAYVKTVLAATGATKVNIVGHSSQGLSSRYVA--AVAPDLVASVTTIGPADRGS 161

Search completed: April 23, 2004, 10:15:21
Job time : 13.398 secs

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OM protein - protein search, using sw model

Run on: April 23, 2004, 10:14:03 ; Search time 35.3571 Seconds

(without alignments)
1407.510 Million cell updates/sec

Title: US-09-905-666A-75

Perfect score: 939
Sequence: 1 EHNPMVVMHIGGASFNAG.....NSQVNSLIKEINGGGLNTN 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_5/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	939	100.0	180	10	US-09-905-666A-75
2	927	98.7	180	10	US-09-905-666A-104
3	925	98.5	180	10	US-09-905-666A-78
4	924	98.4	180	10	US-09-905-666A-98
5	923	98.3	180	10	US-09-905-666A-76
6	923	98.3	180	10	US-09-905-666A-108
7	922	98.2	180	10	US-09-905-666A-87
8	920	98.0	180	10	US-09-905-666A-77
9	920	98.0	212	10	US-09-905-666A-58
10	920	98.0	212	10	US-09-905-666A-59
11	920	98.0	212	13	US-10-028-247-4
12	919	97.9	180	10	US-09-905-666A-99
13	917	97.7	180	10	US-09-905-666A-82
14	917	97.7	180	10	US-09-905-666A-107
15	914	97.3	180	10	US-09-905-666A-102

16	913	97.2	180	10	US-09-905-666A-103	Sequence 103, App
17	913	97.2	180	10	US-09-905-666A-105	Sequence 105, App
18	913	97.2	212	10	US-09-905-666A-62	Sequence 62, App
19	912	97.1	180	10	US-09-905-666A-81	Sequence 81, App
20	911	97.0	180	10	US-09-905-666A-100	Sequence 100, App
21	911	97.0	180	10	US-09-905-666A-101	Sequence 101, App
22	909	96.8	212	10	US-09-905-666A-55	Sequence 55, App
23	909	96.8	212	10	US-09-905-666A-61	Sequence 61, App
24	907	96.6	180	10	US-09-905-666A-97	Sequence 97, App
25	906	96.5	180	10	US-09-905-666A-86	Sequence 86, App
26	906	96.5	180	10	US-09-905-666A-88	Sequence 88, App
27	906	96.5	212	10	US-09-905-666A-60	Sequence 60, App
28	905	96.4	180	10	US-09-905-666A-94	Sequence 94, App
29	904	96.3	180	10	US-09-905-666A-106	Sequence 106, App
30	902	96.1	180	10	US-09-905-666A-80	Sequence 80, App
31	902	96.1	180	10	US-09-905-666A-84	Sequence 84, App
32	901	96.0	180	10	US-09-905-666A-85	Sequence 85, App
33	897	95.5	180	10	US-09-905-666A-83	Sequence 83, App
34	895	95.3	180	10	US-09-905-666A-96	Sequence 96, App
35	891	94.9	180	10	US-09-905-666A-89	Sequence 89, App
36	889	94.7	180	10	US-09-905-666A-95	Sequence 95, App
37	887	94.5	180	10	US-09-905-666A-90	Sequence 90, App
38	887	94.5	180	10	US-09-905-666A-93	Sequence 93, App
39	886	94.4	212	10	US-09-905-666A-69	Sequence 69, App
40	882	93.9	212	10	US-09-905-666A-63	Sequence 63, App
41	881	93.8	180	10	US-09-905-666A-91	Sequence 91, App
42	881	93.8	212	10	US-09-905-666A-56	Sequence 56, App
43	880	93.7	180	10	US-09-905-666A-92	Sequence 92, App
44	872	92.9	212	10	US-09-905-666A-70	Sequence 70, App
45	869	92.5	212	10	US-09-905-666A-68	Sequence 68, App

ALIGNMENTS

RESULT 1
US-09-905-666A-75
; Sequence 75, Application US/09905666A
; Publication No: US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.310US
; CURRENT APPLICATION NUMBER: US/09905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 75
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-905-666A-75

Query Match 100.0%; Score 939; DB 10; Length 180;
Best Local Similarity 100.0%; Pred. No. 6,le-93;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EHNPMVVMHIGGASFNAGIKSYLVSGWGRGKLYAVDFWDKTGTNNYNGPVLRSFVKK 60
Db 1 EHNPMVVMHIGGASFNAGIKSYLVSGWGRGKLYAVDFWDKTGTNNYNGPVLRSFVKK 60
QY 61 VLDETGAQKVDIVAHSMGGANTLYIYIKLGDGKNKVENVTLLGGTNRSTTSKALGTDPNQ 120
Db 61 VLDETGAQKVDIVAHSMGGANTLYIYIKLGDGKNKVENVTLLGGTNRSTTSKALGTDPNQ 120

Qy	121	KILYTSYSSADMIWNYLSKLDGAKNQVIEGVGHIGILMNSQVNSLKEGLNGGGLNTN	180
Db	121	KILYTSYSSADMIWNYLSKLDGAKNQVIEGVGHIGILMNSQVNSLKEGLNGGGLNTN	180

RESULT 2

```

US-09-905-666A-104
; Sequence 104, Application US/09905666A
; Publication No. US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINGSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.310US
; CURRENT APPLICATION NUMBER: US/09/905.666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 180
; TYPE: PRI
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-905-666A-104

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RESULT 3

```

RES001 3
US-09-905-666A-78
; Sequence 78, Application US/09905666A
; Publication NO. US20030096390A1
; GENERAL INFORMATION:
;
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.310US
; CURRENT APPLICATION NUMBER: US/09/905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2003-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

```

RESULT 5

RESUME 3
US-09-905-666A-76
; Sequence 76, Application US/09905666A
; Publication No. US2003009390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT

; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.310US
; CURRENT APPLICATION NUMBER: US/09/905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-905-666A-76

Query Match
Best Local Similarity 98.3%; Score 923; DB 10; Length 180;
Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EHNPMVVMHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKK 60
DB 1 EHNPMVVMHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKD 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLDGKNKVENVTLLGGTNRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLDGKNKVENVTLLGGTNRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

RESULT 6
US-09-905-666A-108
; Sequence 108, Application US/09905666A
; Publication No. US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.310US
; CURRENT APPLICATION NUMBER: US/09/905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-905-666A-108

Query Match
Best Local Similarity 98.3%; Score 923; DB 10; Length 180;
Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EHNPMVVMHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKK 60
DB 1 EHNPMVVMHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKQ 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLDGKNKVENVTLLGGTNRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLDGKNKVENVTLLGGTNRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

DB 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLDGKNKVENVTLLGGTNRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

RESULT 7
US-09-905-666A-87
; Sequence 87, Application US/09905666A
; Publication No. US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.310US
; CURRENT APPLICATION NUMBER: US/09/905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-905-666A-87

Query Match
Best Local Similarity 98.2%; Score 922; DB 10; Length 180;
Matches 175; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EHNPMVVMHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKK 60
DB 1 EHNPMVVMHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKQ 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLDGKNKVENVTLLGGTNRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLDGKNKVENVTLLGGTNRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

RESULT 8
US-09-905-666A-77
; Sequence 77, Application US/09905666A
; Publication No. US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.310US
; CURRENT APPLICATION NUMBER: US/09/905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-905-666A-77

Query Match 98.0%; Score 920; DB 10; Length 180;
Best Local Similarity 97.2%; Pred. No. 6.5e-91;
Matches 175; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKK 60
DB 1 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKK 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTGTTNRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTGTTNRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNQVHGCVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNQVHGCVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

RESULT 9
US-09-905-666A-58
Sequence 58, Application US/09905666A
Publication No. US20030096390A1
GENERAL INFORMATION:
APPLICANT: GIVER, LORRAINE J.
APPLICANT: MINSHULL, JEREMY
APPLICANT: VOGEL, KURT
TITLE OF INVENTION: NOVEL LIPASE GENES
FILE REFERENCE: 0184.310US
CURRENT APPLICATION NUMBER: US/09/905.666A
CURRENT FILING DATE: 2002-10-15
PRIOR FILING DATE: 2000-07-13
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/300,378
PRIOR FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 111
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 58
LENGTH: 212
TYPE: PRT
ORGANISM: Bacillus lentus
US-09-905-666A-58

Query Match 98.0%; Score 920; DB 10; Length 212;
Best Local Similarity 97.2%; Pred. No. 8.5e-91;
Matches 175; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKK 60
DB 33 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKK 92
QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTGTTNRSTTSKALPGTDPNQ 120
DB 93 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTGTTNRSTTSKALPGTDPNQ 152
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNQVHGCVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 153 KILYTSIYSSADMIVMNYLSKLDGAKNQVHGCVGHIGLLMNSQVNSLIKEGLNGGLNTN 212

RESULT 10
US-09-905-666A-59
Sequence 59, Application US/09905666A
Publication No. US20030096390A1
GENERAL INFORMATION:
APPLICANT: GIVER, LORRAINE J.
APPLICANT: MINSHULL, JEREMY
APPLICANT: VOGEL, KURT
TITLE OF INVENTION: NOVEL LIPASE GENES
FILE REFERENCE: 0184.310US

CURRENT APPLICATION NUMBER: US/09/905.666A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/217,954
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/300,378
PRIOR FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 111
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 59
LENGTH: 212
TYPE: PRT
ORGANISM: Bacillus circulans
US-09-905-666A-59

Query Match 98.0%; Score 920; DB 10; Length 212;
Best Local Similarity 97.2%; Pred. No. 8.5e-91;
Matches 175; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKK 60
DB 33 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKK 92
QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTGTTNRSTTSKALPGTDPNQ 120
DB 93 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTGTTNRSTTSKALPGTDPNQ 152
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNQVHGCVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 153 KILYTSIYSSADMIVMNYLSKLDGAKNQVHGCVGHIGLLMNSQVNSLIKEGLNGGLNTN 212

RESULT 11
US-10-028-247-4
Sequence 4, Application US/10028247
Publication No. US20020150594A1
GENERAL INFORMATION:
APPLICANT: Goldman, Stanley
APPLICANT: Iathrop, Stephanie J.
APPLICANT: Longchamp, Pascal F.
APPLICANT: Whalen, Robert G.
APPLICANT: Maxygen, Inc.
TITLE OF INVENTION: Methods and Compositions for Developing Spore Display
TITLE OF INVENTION: Systems for Medicinal and Industrial Applications
FILE REFERENCE: 18097A-033520US
CURRENT APPLICATION NUMBER: US/10/028.247
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/214,161
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 09/892,208
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 4
LENGTH: 212
TYPE: PRT
ORGANISM: Bacillus circulans
FEATURE: lipase 396
OTHER INFORMATION: lipase 396
US-10-028-247-4

Query Match 98.0%; Score 920; DB 13; Length 212;
Best Local Similarity 97.2%; Pred. No. 8.5e-91;
Matches 175; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKK 60
DB 33 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKK 92
QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTGTTNRSTTSKALPGTDPNQ 120
DB 93 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTGTTNRSTTSKALPGTDPNQ 152
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNQVHGCVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

US-09-905-666A-82

Matches	174;	Conservative	4;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1	EHNPMVHHGTCGASFNAGIKSYILVSGWSEKLYAYDFWDKGTGNTYNNGPVLSEFVKK	60						
Ddb	1	EHNPMVHHGTCGASFNAGIKSYILVSGWSEKLYAYDFWDKGTGNTYNNGPVLSEFVKK	60						
Qy	61	VLDEGTAKKVDIVAHSMGGANTLYYIKNLGGNKVENVVTLGTTNRSTTSKALPGTDPNQ	120						
Ddb	61	VLDEGTAKKVDIVAHSMGGANTLYYIKNLGGNKIENVVTLGGANRLTTSKALPGTDPNQ	120						
Qy	121	KILYTSYSSADMIYVNYLSKLDGAKNQVIGHGVGHIGLLMRISOVNSLIKEGLNGGGLNTN	180						
Ddb	121	KILYTSYSSADMIYVNYLSKLDGAKNQVIGHGVGHIGLLMRISOVNSLIKEGLNGGGLNTN	180						

RESULT 14
 US-09-905-666A-107
 ; Sequence 107, Application US/09905666A
 ; Publication No. US20030096390A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GIVER, LORRAINE J.
 ; APPLICANT: MINSHULL, JEREMY
 ; APPLICANT: VOGEL, KURT
 ; TITLE OF INVENTION: NOVEL LIPASE GENES
 ; FILE REFERENCE: 0184.310US
 ; CURRENT APPLICATION NUMBER: US/09/905,666A
 ; CURRENT FILING DATE: 2002-10-15

```

, PRIOR APPLICATION NUMBER: 60/217,954
, PRIOR FILING DATE: 2000-07-13
, PRIOR APPLICATION NUMBER: 60/300,378
, PRIOR FILING DATE: 2001-06-21
, NUMBER OF SEQ ID NOS: 11
, SOFTWARE: Patentin Ver. 2.1
, SEQ ID NO 107
, LENGTH: 180
, TYPE: PRT
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: Synthetic
, OTHER INFORMATION: peptide
US-09-905-666A-107
Query Watch 97.7% Score 917; DB 10; Length 180;

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Matches 176; Conservative 1; Mismatches 3; Indels 0; Gaps 0
QY 1 EHNPPVVMVHAGIGASFNFAIGIKSYLVQGSWSRDKLYAVDFWDKTGTNYNNGPVLRSRVKK 60
Db 1 EHNPPVVMVHAGIGASFNFAIGIKSYLVQGSWSRDKLYAVDFWDKTGTNYNNGPVLRSRVQK 60
QY 61 VLDETGAKKVDIVVAHSMGGANTLYYIKNLDGGKNKVNVTLLGTNRSTTSKALPGTDPNQ 120
Db 61 VLDETGAKKVDIVVAHSMGGANTLYYIKNLDGGKNKVNVTLLGTNRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYASADMIVMNLYLSKLDGAKNVQIHGVGHIGLLMNSOVNSLIKEGLNGGGNTN 180
Db 121 KILYTSIYASADMIVMNLYLSKLDGAKNVQIHGVGHIGLLMNSOVNSLIKEGLNGGGQNTN 180

RESULT 15
US-09-905-666A-102
; Sequence 102, Application US/09905666A
; Publication No. US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.3100S

```

; CURRENT APPLICATION NUMBER: US/09/905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-905-666A-102

Query Match 97.3%; Score 914; DB 10; Length 180;
Best Local Similarity 96.7%; Pred. No. 3e-90;
Matches 174; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EHNPPVVMVHGIGGASFNFAIGIKSYLSQGSRGKLYAVDFWDTGTNTYNNNGFVLSRFVKK 60
Db 1 EHNPPVVMVHGIGGASFNFAIGIKSYLSQGSRGKLYAVDFWDTGTNTYNNNGFVLSRFVKK 60
QY 61 VLDETGAKKVDIVAHSGGANTLYIKNLGGKNKVENVTLGGTNRSTTSKALPGTDENQ 120
Db 61 VLDETGAKKVDIVAHSGGANTLYIKNLGGKNKVENVTLGGTNRSTTSKALPGTDENQ 120
QY 121 KILYTSYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
Db 121 KILYTSYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180

Search completed: April 23, 2004, 10:23:29
Job time : 36.3571 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 10:08:37 ; Search time 15.1531 Seconds
(without alignments)
613.254 Million cell updates/sec

Title: US-09-905-666A-75
Perfect score: 939
Sequence: 1 ENHVVVHVGICGASFNFAG.....NSQVNSLIKEGLNGGLNTN 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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6: /cgn2_6/prodata/2/aaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	747	79.6	213	1	US-07-930-678-2
2	129.5	13.8	358	1	US-08-034-650-10
3	129.5	13.8	358	1	US-08-449-015-10
4	117.5	12.5	363	3	US-08-978-589A-2
5	117.5	12.5	363	3	US-09-336-601-1
6	117.5	12.5	363	4	US-09-219-120-2
7	110.5	11.8	296	4	US-09-543-681A-7771
8	110.5	11.8	364	1	US-08-400-422-3
9	110.5	11.7	351	4	US-09-252-991A-27337
10	107.5	11.4	318	4	US-09-489-039A-7418
11	97.5	10.4	690	4	US-09-134-001C-4568
12	95.5	10.2	699	4	US-09-134-001C-4054
13	94.5	10.1	299	4	US-09-584-568C-5
14	93.5	10.0	292	4	US-09-134-001C-3301
15	92.5	9.9	308	4	US-09-584-568C-8
16	92	9.8	316	4	US-09-107-532A-4594
17	90.5	9.6	325	4	US-09-328-352-6196
18	87.5	9.3	1216	4	US-09-134-000C-5130
19	86.5	9.2	388	1	US-08-232-519-2
20	86.5	9.2	388	1	US-08-456-956-2
21	85	9.2	264	4	US-09-134-001C-5592
22	85	9.2	1053	4	US-09-062-126-10
23	85.5	9.1	453	4	US-09-328-352-5069
24	85	9.1	652	4	US-09-134-001C-3517
25	84.5	9.0	416	4	US-09-489-039A-8245
26	84	8.9	262	2	US-08-602-359A-35
27	83.5	8.9	315	4	US-09-584-568C-2

28 83 8.8 284 4 US-09-134-001C-2927 Sequence 2927, Ap
29 83 8.8 491 4 US-09-134-001C-3510 Sequence 3510, Ap
30 83 8.8 503 4 US-09-562-737-64 Sequence 64, Appl
31 82.5 8.8 236 4 US-09-134-000C-5155 Sequence 5155, Ap
32 82 8.7 734 4 US-09-489-039A-9951 Sequence 9951, Ap
33 82 8.7 1059 4 US-09-489-039A-10044 Sequence 10044, A
34 81.5 8.7 277 3 US-09-111-556A-3 Sequence 3, Appli
35 81.5 8.7 277 3 US-08-360-758-3 Sequence 3, Appli
36 81 8.6 313 3 US-08-732-412-2 Sequence 2, Appli
37 81 8.6 671 2 US-08-737-716-13 Sequence 13, Appli
38 81 8.6 700 4 US-09-620-412C-345 Sequence 345, App
39 81 8.6 700 4 US-09-598-419-345 Sequence 345, App
40 81 8.6 1752 4 US-09-556-877-180 Sequence 180, App
41 81 8.6 1752 4 US-09-620-412C-180 Sequence 180, App
42 81 8.6 1752 4 US-09-598-419-180 Sequence 180, App
43 80.5 8.6 464 4 US-09-711-164-441 Sequence 441, App
44 80.5 8.6 766 4 US-09-540-236-2515 Sequence 2515, Ap
45 80.5 8.6 1221 4 US-09-107-532A-3959 Sequence 3959, Ap

ALIGNMENTS

RESULT 1
US-07-930-678-2
; Sequence 2, Application US/07930678
; Patent No. 5427936
; GENERAL INFORMATION:
; APPLICANT: MOELLER, Bernhard
; APPLICANT: VETTER, Roman
; APPLICANT: WILKE, Detlef
; APPLICANT: FOULLOIS, Birgit
; TITLE OF INVENTION: Alkaline Bacillus Lipases, Coding DNA
; TITLE OF INVENTION: Sequences Therefor and Bacilli, Which Produce These
; TITLE OF INVENTION: Lipases
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/930,678
; FILING DATE: 19921013
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP91/00664
; FILING DATE: 08-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 40 12 070.8
; FILING DATE: 14-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, J.D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 16877/318/KACH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-930-678-2

Query Match 79.6%; Score 747; DB 1; Length 213;
Best Local Similarity 78.3%; Pred. No. 5.2e-73;
Matches 141; Conservative 17; Mismatches 22; Indels 0; Gaps 0;

QY 1 EHNFWMHGIGGASFNFAIKSYLVSGWSEKLYAVDFWDTGTNNYNGPVLRSFYKK 60
DB 34 EHNFWMHGIGGASFNFAIKSYLVSGWSEKLYAVDFWDTGTNNYNGPVLRSFYKK 93
QY 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLGGKKNVNTLGGTNRSTTSKALPCTDPNQ 120
DB 94 VLDKTKGAKKVDIVAHSMGGANTLYYIKNLGGKKNVNTLGGTNRSTTSKALPCTDPNQ 153
QY 121 KILYTSYSSADMVWYVYLSKLDGAKVQIHGVGHIGLMMSONVSLIKEGLNGGLNTN 180
DB 154 KILYTSYSSADLIYVNSLSLIGARNILIHGVGHIGLTSQVKGYIKEGLNGGGQNTN 213

RESULT 2
US-08-034-650-10
; Sequence 10, Application US/08034650
; Patent No. 5641671
; GENERAL INFORMATION:
; APPLICANT: BOS, Jannetje W.
; APPLICANT: FRENKEN, Leon G.
; APPLICANT: VERRIJS, Cornelis T.
; APPLICANT: VISSER, Christiaan
; TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
; TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/034,650
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 07/727,235
; FILING DATE: 03-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: PNK/5970/91731
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-034-650-10

Query Match 13.8%; Score 129.5; DB 1; Length 358;
Best Local Similarity 34.8%; Pred. No. 9.7e-06;
Matches 40; Conservative 16; Mismatches 42; Indels 17; Gaps 6;

QY 4 PYVMWHGIGGASFNFA-----GIKSYLVSGWSEKLYAVD---FWDKGTNNYNGPV 53
DB 49 PVILVHGLAGTD-KFANVVDYWGIDQLQSHG---AKVYVANLSGFQSDGPN-GRGEQ 103
QY 54 LSEFVKKVLDETGAKKVDIVAHSMGGANTLYYIKNLGGKKNVNTLGGTNRST 108
DB 104 LLAYVKQVLAATGATKVNLIHSGQLTSRYVA--AVAPQLVASVTITGTPHRS 156

RESULT 3
US-08-449-015-10
; Sequence 10, Application US/08449015
; Patent No. 5804409
; GENERAL INFORMATION:
; APPLICANT: BOS, Jannetje W.
; APPLICANT: FRENKEN, Leon G.
; APPLICANT: VERRIJS, Cornelis T.
; APPLICANT: VISSER, Christiaan
; TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
; TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,015
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 07/727,235
; FILING DATE: 03-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: PNK/5970/91731
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-015-10

Query Match 13.8%; Score 129.5; DB 1; Length 358;
Best Local Similarity 34.8%; Pred. No. 9.7e-06;
Matches 40; Conservative 16; Mismatches 42; Indels 17; Gaps 6;

QY 4 PYVMWHGIGGASFNFA-----GIKSYLVSGWSEKLYAVD---FWDKGTNNYNGPV 53
DB 49 PVILVHGLAGTD-KFANVVDYWGIDQLQSHG---AKVYVANLSGFQSDGPN-GRGEQ 103
QY 54 LSEFVKKVLDETGAKKVDIVAHSMGGANTLYYIKNLGGKKNVNTLGGTNRST 108
DB 104 LLAYVKQVLAATGATKVNLIHSGQLTSRYVA--AVAPQLVASVTITGTPHRS 156

RESULT 4
US-08-978-589A-2
; Sequence 2, Application US/08978589A
; Patent No. 6087145
; GENERAL INFORMATION:
; APPLICANT: ISHII, Takeshi
; APPLICANT: MITSUDA, Satoshi
; TITLE OF INVENTION: ESTERASE GENE AND ITS USE

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VIRGINIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 22040
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,589A
FILING DATE: 26-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 20-4336P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-978-589A-2

Query Match 12.5%; Score 117.5; DB 3; Length 363;
Best Local Similarity 29.8%; Pred. No. 0.0002;
Matches 39; Conservative 21; Mismatches 46; Indels 25; Gaps 8;
QY 4 PVMVHGIGGASFNAGIKSYLVSGWSR-----GKLYAVD---FWDKTGTNYNNG 51
DB 54 PIILVHGLTGTD-KYGGVVEY-----WYRIPEDLRAHGAAYIVANLSGFQSDGPN-GRG 106
QY 52 PVLRSRVKKVLDGTGAKKVDIVAHSMGGANTLYIYIKNLDGKNKVENVVTLG----GTNRS 107
DB 107 EQLLAFVKQVLAATGAQKNLIGHSGGGL-TSRYVASV-APELVASVTTISTPHWGSQFA 164
QY 108 TTSKALPGTDP 118
DB 165 DFVQQLQTD 175

RESULT 5
US-09-336-601-1
; Sequence 1, Application US/09336601
; Patent No. 6184008
; GENERAL INFORMATION:
; APPLICANT: OHTA, Hiromichi
; APPLICANT: SUGAI, Takeshi
; APPLICANT: ISHII, Takeshi
; APPLICANT: MITSUDA, Satsoshi
; TITLE OF INVENTION: PRODUCTION OF OPTICALLY ACTIVE SPHINGOID COMPOUND
; FILE REFERENCE: 2185-349P
; CURRENT APPLICATION NUMBER: US/09/336,601
; EARLIER FILING DATE: 1999-06-21
; EARLIER APPLICATION NUMBER: 09/034,007
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 363
; TYPE: PRT
; ORGANISM: E. coli JM 109/pAL 612 strain
US-09-336-601-1

Query Match 12.5%; Score 117.5; DB 3; Length 363;

Best Local Similarity 29.8%; Pred. No. 0.0002;
Matches 39; Conservative 21; Mismatches 46; Indels 25; Gaps 8;
QY 4 PVMVHGIGGASFNAGIKSYLVSGWSR-----GKLYAVD---FWDKTGTNYNNG 51
DB 54 PIILVHGLTGTD-KYGGVVEY-----WYRIPEDLRAHGAAYIVANLSGFQSDGPN-GRG 106
QY 52 PVLRSRVKKVLDGTGAKKVDIVAHSMGGANTLYIYIKNLDGKNKVENVVTLG----GTNRS 107
DB 107 EQLLAFVKQVLAATGAQKNLIGHSGGGL-TSRYVASV-APELVASVTTISTPHWGSQFA 164
QY 108 TTSKALPGTDP 118
DB 165 DFVQQLQTD 175

RESULT 6
US-09-219-120-2
; Sequence 2, Application US/09219120
; Patent No. 6472189
; GENERAL INFORMATION:
; APPLICANT: TAKESHI, Ishii
; APPLICANT: SATOSHI, Mitsuda
; TITLE OF INVENTION: ESTERASE GENE AND ITS USE
; FILE REFERENCE: 20-4336P
; CURRENT APPLICATION NUMBER: US/09/219,120
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
US-09-219-120-2

Query Match 12.5%; Score 117.5; DB 4; Length 363;
Best Local Similarity 29.8%; Pred. No. 0.0002;
Matches 39; Conservative 21; Mismatches 46; Indels 25; Gaps 8;
QY 4 PVMVHGIGGASFNAGIKSYLVSGWSR-----GKLYAVD---FWDKTGTNYNNG 51
DB 54 PIILVHGLTGTD-KYGGVVEY-----WYRIPEDLRAHGAAYIVANLSGFQSDGPN-GRG 106
QY 52 PVLRSRVKKVLDGTGAKKVDIVAHSMGGANTLYIYIKNLDGKNKVENVVTLG----GTNRS 107
DB 107 EQLLAFVKQVLAATGAQKNLIGHSGGGL-TSRYVASV-APELVASVTTISTPHWGSQFA 164
QY 108 TTSKALPGTDP 118
DB 165 DFVQQLQTD 175

RESULT 7
US-09-543-681A-7771
; Sequence 7771, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7771
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7771

Query Match 11.8%; Score 110.5; DB 4; Length 296;

Best Local Similarity 31.6%; Pred. No. 0.00085;
Matches 36; Conservative 15; Mismatches 44; Indels 19; Gaps 5;
QY 4 PVMVHGIGGASFN-----PAGIKSYLVQGS--RGKLYAVDFWDXCTGTTNNNGPVL 54
DB 15 PIVLHGLAG--FNEIVGFYFGIADALRQDGHQVFTASLAFN-----SNEVRGKQL 66
QY 55 SRFVKKVLDGTGAKKVDIVAHSMGGANTLYIKNLDDGKNKVENVTLGTTNRST 108
DB 67 WQFVTLQETQAKKVNIGHGQGLACRYAANYP--DSVASVTSINGVNHGS 118

RESULT 8
US-08-400-422-3
; Sequence 3, Application US/08400422
; Patent No. 5681715
; GENERAL INFORMATION:
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Diderichsen, Boerge Krag
; APPLICANT: Buckley, Catherine M.
; APPLICANT: Hobson, Audrey
; APPLICANT: McConnell, David J.
; TITLE OF INVENTION: A process for the preparation of an active
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56817150 No. 5681715disk of No. 5681715th America, Inc.
; STREET: 405 Lexington Avenue, 62nd floor
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/400,422
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/038,763
; FILING DATE: 25-MAR-1993
; APPLICATION NUMBER: PCT/DK91/00402
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK92/00391
; FILING DATE: 18-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3663.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 364 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Pseudomonas cepacia
; STRAIN: DSM 3401
US-08-400-422-3

Query Match 11.8%; Score 110.5; DB 1; Length 364;
Best Local Similarity 31.0%; Pred. No. 0.0011;

Matches 35; Conservative 16; Mismatches 45; Indels 17; Gaps 6;
QY 4 PVMVHGIGGASFNAGIKSY-----LVSGWSRGKLYAVD---FWDKCTGTYNNGPV 53
DB 54 PIVLHGLTGT-D-KVAGVLEWYQIEDLQQEG---ATVIVANLSGFQDDGPN-GRGEQ 108
QY 54 LSRFVKVLDGTGAKKVDIVAHSMGGANTLYIKNLDDGKNKVENVTLGTTNR 106
DB 109 LLAYVKTVAATGATKVNLVGHQGLTSRYVA--AVAPDLVASVTITGTPHR 159

RESULT 9
US-09-252-991A-27337
; Sequence 27337, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27337
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27337

Query Match 11.7%; Score 110; DB 4; Length 351;
Best Local Similarity 25.3%; Pred. No. 0.0012;
Matches 42; Conservative 30; Mismatches 54; Indels 40; Gaps 7;

QY 4 PVMVHGIGGASFNAGIKSYLVSGWSRGKLYAVDFW-----DKTG----- 45
DB 75 PIVLSHGLFG--FKSVG-----PVDYWHAIVPALEKDGAKVFATSQSPV 116
QY 46 -TNNNGPVLRSFVKVLDGTGAKKVDIVAHSMGGANTLYIKNLDDGKNKVENVTLGTT 104
DB 117 NSNEVRGEQLLAQVEEVLALTGAEKVNLIGHSGQGM-TVRYVAGV-APQLVASVTITGTP 174
QY 105 NRST-TSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQ 149
DB 175 HKGTFVADAVTGFSEFLGPIGTEVIASAVEALFVVVDIVDGEWVK 220

RESULT 10
US-09-489-039A-7418
; Sequence 7418, Application US/09489039A
; Patent No. 6610838
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7418
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7418

Query Match 11.4%; Score 107.5; DB 4; Length 318;
Best Local Similarity 26.9%; Pred. No. 0.002;
Matches 46; Conservative 30; Mismatches 64; Indels 31; Gaps 8;


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; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3301
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3301

Query Match      10.0%; Score 93.5; DB 4; Length 292;
Best Local Similarity 21.8%; Pred. No. 0.058;
Matches 43; Conservative 26; Mismatches 47; Indels 81; Gaps 8;

QY 6 VVHVGIGGASFNFAGIKSYLVSQGW-----SEGKLY-----A 37
Db 52 LFLHGYGGSERS-----ETFMVKQALNKNVINEVITARVSSEKGYFDKLSSEDAANPIVK 107
QY 38 VDFWD-KTGTNYNGPVLRSFVKVLDGTGAKKYDIAVHSMGGANTLYIKNLDDGKNKE 96
Db 108 VEFKDKTKGNFKENAYWIKVELSKSQFG:QQNFVCHSMGNISPAFYMKNY----- 160
QY 97 NVVTILGGRNRTTSKALPCTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHI 156
Db 161 -----GDD-----RHLPLQ-----KKEVNIAGVING 181
QY 157 GLMNSQVNSLI--KEG 171
Db 182 ILMNENVEIIVDKQG 198
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```
RESULT 15
US-09-584-568C-8
; Sequence 8, Application US/09584568C
; Patent No. 6500657
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria, Alexandra et al.
; TITLE OF INVENTION: 33167, A NOVEL HUMAN HYDROLASE AND USES THEREFOR
; FILE REFERENCE: MNI-140
; CURRENT APPLICATION NUMBER: US/09/584,568C
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/193,954
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-584-568C-8
```

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Query Match      9.9%; Score 92.5; DB 4; Length 308;
Best Local Similarity 26.4%; Pred. No. 0.08;
Matches 23; Conservative 23; Mismatches 36; Indels 5; Gaps 3;

QY 4 PVVWVGIGGASFNFAGIKSYLVSQGWSRGKLYAVD---FWDXTGTNYNGPVLRSFVKK 60
Db 54 PLLTYHGLFGSKQNRGISKALVRK-VSR-KYVADVRNHGSPHSSVHNSKANGSEDURL 111
QY 61 VLDETGAKKYDIAVHSMGGANTLYIYIK 87
Db 112 FMEQRSHFNAACMGHSGGERSMNYFAR 138
```

Search completed: April 23, 2004, 10:14:40
Job time : 16.1531 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 10:01:12 ; Search time 46.3776 Seconds
(without alignments)
1096.620 Million cell updates/sec

Title: US-09-305-666A-75
Perfect score: 939
Sequence: 1 EBNPVVHVGIGGASFNFAG.....NSQVNSLIKEGLNGGLNTN 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1380s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	939	100.0	180	5	AAU83861 Bacillus
2	927	98.7	180	5	AAU83890 Bacillus
3	925	98.5	180	5	AAU83864 Bacillus
4	924	98.4	180	5	AAU83884 Bacillus
5	923	98.3	180	5	AAU83862 Bacillus
6	923	98.3	180	5	AAU83894 Bacillus
7	922	98.2	180	5	AAU83873 Bacillus
8	920	98.0	180	5	AAU83863 Bacillus
9	920	98.0	212	5	AAU83845 Bacillus
10	920	98.0	212	5	AAU83844 Bacillus
11	919	97.9	180	5	AAU83885 Bacillus
12	917	97.7	180	5	AAU83868 Bacillus
13	917	97.7	180	5	AAU83893 Bacillus
14	914	97.3	180	5	AAU83888 Bacillus
15	913	97.2	180	5	AAU83889 Bacillus
16	913	97.2	180	5	AAU83891 Bacillus
17	913	97.2	212	5	AAU83848 Bacillus
18	912	97.1	180	5	AAU83867 Bacillus
19	911	97.0	180	5	AAU83887 Bacillus
20	911	97.0	180	5	AAU83886 Bacillus
21	909	96.8	212	5	AAU83847 Bacillus
22	909	96.8	212	5	AAU83841 Bacillus
23	907	96.6	180	5	AAU83883 Bacillus
24	906	96.5	180	5	AAU83874 Bacillus
25	906	96.5	180	5	AAU83872 Bacillus

26	906	96.5	212	5	AAU83846	Bacillus
27	905	96.4	180	5	AAU83880	Bacillus
28	904	96.3	180	5	AAU83892	Bacillus
29	902	96.1	180	5	AAU83870	Bacillus
30	902	96.1	180	5	AAU83866	Bacillus
31	901	96.0	180	5	AAU83871	Bacillus
32	897	95.5	180	5	AAU83869	Bacillus
33	895	95.3	180	5	AAU83882	Bacillus
34	891	94.9	180	5	AAU83875	Bacillus
35	889	94.7	180	5	AAU83881	Bacillus
36	887	94.5	180	5	AAU83876	Bacillus
37	887	94.5	180	5	AAU83879	Bacillus
38	886	94.4	212	5	AAU83855	Bacillus
39	882	93.9	212	5	AAU83849	Bacillus
40	881	93.8	180	5	AAU83877	Bacillus
41	881	93.8	212	5	AAU83842	Bacillus
42	880	93.7	180	5	AAU83878	Bacillus
43	872	92.9	212	5	AAU83856	Bacillus
44	869	92.5	212	5	AAU83854	Bacillus
45	862	91.8	212	5	AAU83843	Bacillus

ALIGNMENTS

RESULT 1

AAU83861
ID AAU83861 standard; protein; 180 AA.

XX AAU83861;

AC
DT 08-MAY-2002 (first entry)

XX
DE Bacillus lipase polypeptide #21.

XX Lipase; Bacillus; animal feed; flavour modification; fat modification;
human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
gastrointestinal lipid related condition; antiinflammatory; respiratory;
gastrointestinal.
XX Synthetic.

XX WO200206457-A2.

XX 24-JAN-2002.

XX 13-JUL-2001; 2001WO-US022160.

XX 13-JUL-2000; 2000US-0217954P.

XX 21-JUN-2001; 2001US-0300378P.

XX (MAXY-) MAXYGEN INC.

XX Giver LJ, Minshull J, Vogel K;

XX WPI; 2002-171805/22.

XX N-PSDB; ABK33839.

XX Nucleic acids encoding lipase enzymes which are useful as supplements in animal feeds, as agents of flavor modification and for treating Crohn's disease and celiac disease.

XX Claim 5; Page 141; 196pp; English.

XX The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other

CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention
XX
XX
SQ Sequence 180 AA;
Query Match 100.0%; Score 939; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 6,5e-87; Indels 0; Gaps 0;
Matches 180; Conservative 0; Mismatches 0;
QY 1 EHNPPVVMVHGIGGASFNAGIKSYLVSGWGRGKLYAVDFWDKTGTNNNGPVLSPFVKK 60
DB 1 EHNPPVVMVHGIGGASFNAGIKSYLVSGWGRGKLYAVDFWDKTGTNNNGPVLSPFVKK 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLGGNKVENVVTLLGGTNRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLGGNKVENVVTLLGGTNRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
RESULT 2
AAU83890
ID AAU83890 standard; protein; 180 AA.
XX
XX
AC AAU83890;
XX
DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polypeptide #50.
XX
KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW Gastrointestinal.
XX
OS Synthetic.
XX
XX WO200206457-A2.
XX
XX PD 24-JAN-2002.
XX
XX PF 13-JUL-2001; 2001WO-US022160.
XX
XX PR 13-JUL-2000; 2000US-0217954P.
XX
XX PR 21-JUN-2001; 2001US-0300378P.
XX
XX PA (MAXY-) MAXYGEN INC.
XX
XX PI Giver LJ, Minshull J, Vogel K;
XX
XX WPI; 2002-171805/22.
XX
XX DR N-PSDB; ABK33883.
XX
XX Nucleic acids encoding lipase enzymes which are useful as supplements in
XX animal feeds, as agents of flavor modification and for treating Crohn's
XX disease and celiac disease.
XX
XX PS Claim 5; Page 145; 196pp; English.
XX
XX The invention relates to new Bacillus lipase enzymes and the nucleic
XX acids encoding them. The lipase polypeptides are useful as supplements in
XX animal feeds, as agents of flavour modification and fat modification in
XX human foodstuffs (e.g. cheese), as agents in the creation of food
XX emulsifiers, as agents for tanning/processing of leather and as cleaning
XX agents. They are also useful for treating Crohn's disease, cystic

CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention
XX
XX
SQ Sequence 180 AA;
Query Match 98.7%; Score 927; DB 5; Length 180;
Best Local Similarity 98.3%; Pred. No. 1.1e-85;
Matches 177; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 EHNPPVVMVHGIGGASFNAGIKSYLVSGWGRGKLYAVDFWDKTGTNNNGPVLSPFVKK 60
DB 1 EHNPPVVMVHGIGGASFNAGIKSYLVSGWGRGKLYAVDFWDKTGTNNNGPVLSPFVKK 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLGGNKVENVVTLLGGTNRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLGGNKVENVVTLLGGTNRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
RESULT 3
AAU83864
ID AAU83864 standard; protein; 180 AA.
XX
XX
AC AAU83864;
XX
DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polypeptide #24.
XX
KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW Gastrointestinal.
XX
OS Synthetic.
XX
XX WO200206457-A2.
XX
XX PD 24-JAN-2002.
XX
XX PF 13-JUL-2001; 2001WO-US022160.
XX
XX PR 13-JUL-2000; 2000US-0217954P.
XX
XX PR 21-JUN-2001; 2001US-0300378P.
XX
XX PA (MAXY-) MAXYGEN INC.
XX
XX PI Giver LJ, Minshull J, Vogel K;
XX
XX WPI; 2002-171805/22.
XX
XX DR N-PSDB; ABK33842.
XX
XX Nucleic acids encoding lipase enzymes which are useful as supplements in
XX animal feeds, as agents of flavor modification and for treating Crohn's
XX disease and celiac disease.
XX
XX PS Claim 5; Page 141-142; 196pp; English.
XX
XX The invention relates to new Bacillus lipase enzymes and the nucleic
XX acids encoding them. The lipase polypeptides are useful as supplements in
XX animal feeds, as agents of flavour modification and fat modification in
XX human foodstuffs (e.g. cheese), as agents in the creation of food
XX emulsifiers, as agents for tanning/processing of leather and as cleaning

CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences AAU83841-AAU83997 represent Bacillus lipase
 CC polypeptides of the invention
 XX
 XX Sequence 180 AA;

Query Match 98.5%; Score 925; DB 5; Length 180;
 Best Local Similarity 97.8%; Pred. No. 1.7e-85;
 Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EHNPPVVMVHGIIGGASFNFAIGIKSYLVSQGWSRGKLYAVDFWDTGTNTYNNNGPVLSEFVVK 60
 DB 1 EHNPPVVMVHGIIGGASFNFAIGIKSYLVSQGWSRGKLYAVDFWDTGTNTYNNNGPVLSEFVVK 60
 QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNVENVTGNTNSTTSKALPGTDPNQ 120
 DB 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNVENVTGNTNSTTSKALPGTDPNQ 120
 QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
 DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180

RESULT 4
 AAU83884
 ID AAU83884 standard; protein; 180 AA.
 AC AAU83884;
 DT 08-MAY-2002 (first entry)
 DE Bacillus lipase polypeptide #44.
 XX Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
 KW gastrointestinal.
 OS Synthetic.
 XX WO200206457-A2.
 PN 24-JAN-2002.
 PD 13-JUL-2001; 2001WO-US022160.
 PF 13-JUL-2000; 2000US-0217954P.
 PR 21-JUN-2001; 2001US-0300378P.
 XX (MAXY-) MAXYGEN INC.
 PA Giver LJ, Minshull J, Vogel K;
 PI WPI; 2002-171805/22.
 DR N-PSDB; ABK33862.
 XX Nucleic acids encoding lipase enzymes which are useful as supplements in
 PT animal feeds, as agents of flavor modification and for treating Crohn's
 PT disease and celiac disease.
 XX Claim 5; Page 144; 196pp; English.

XX The invention relates to new Bacillus lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in
 CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food

CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences AAU83841-AAU83997 represent Bacillus lipase
 CC polypeptides of the invention
 XX
 XX Sequence 180 AA;

Query Match 98.4%; Score 924; DB 5; Length 180;
 Best Local Similarity 97.8%; Pred. No. 2.2e-85;
 Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EHNPPVVMVHGIIGGASFNFAIGIKSYLVSQGWSRGKLYAVDFWDTGTNTYNNNGPVLSEFVVK 60
 DB 1 EHNPPVVMVHGIIGGASFNFAIGIKSYLVSQGWSRGKLYAVDFWDTGTNTYNNNGPVLSEFVVK 60
 QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNVENVTGNTNSTTSKALPGTDPNQ 120
 DB 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNVENVTGNTNSTTSKALPGTDPNQ 120
 QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
 DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180

RESULT 5
 AAU83862
 ID AAU83862 standard; protein; 180 AA.
 AC AAU83862;
 DT 08-MAY-2002 (first entry)
 DE Bacillus lipase polypeptide #22.
 XX Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
 KW gastrointestinal.
 OS Synthetic.
 XX WO200206457-A2.
 PN 24-JAN-2002.
 PD 13-JUL-2001; 2001WO-US022160.
 PF 13-JUL-2000; 2000US-0217954P.
 PR 21-JUN-2001; 2001US-0300378P.
 XX (MAXY-) MAXYGEN INC.
 PA Giver LJ, Minshull J, Vogel K;
 PI WPI; 2002-171805/22.
 DR N-PSDB; ABK33840.
 XX Nucleic acids encoding lipase enzymes which are useful as supplements in
 PT animal feeds, as agents of flavor modification and for treating Crohn's
 PT disease and celiac disease.
 XX Claim 5; Page 141; 196pp; English.

XX The invention relates to new Bacillus lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in
 CC animal feeds, as agents of flavour modification and fat modification in

CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
 CC polypeptides of the invention
 XX
 SQ Sequence 180 AA;

Query Match 98.3%; Score 923; DB 5; Length 180;
 Best Local Similarity 97.8%; Pred. No. 2.7e-85;
 Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EHNPPVVMVHGIGGASFNPAIGIKSYLVSGWSRGKLYAVDFWDKTGTNTNNGPVLRSFVK 60
 DB 1 EHNPPVVMVHGIGGASFNPAIGIKSYLVSGWSRGKLYAVDFWDKTGTNTNNGPVLRSFVK 60
 QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLGGKNKVENVTLLGGTNRSTTSKALPGTDPNQ 120
 DB 61 VLDETGAKKVDIVAHSMGGANTLYIKNLGGKNKVENVTLLGGTNRSTTSKALPGTDPNQ 120
 QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
 DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

RESULT 6
 AAU83894
 ID AAU83894 standard; protein; 180 AA.
 AC AAU83894;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Bacillus lipase polypeptide #54.
 XX
 KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
 XX
 OS Synthetic.
 XX
 FN WO200206457-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 13-JUL-2001; 2001WO-US022160.
 XX
 PR 13-JUL-2000; 2000US-0217954P.
 PR 21-JUN-2001; 2001US-0300378P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 XX Giver LJ, Minshull J, Vogel K;
 PI
 XX WPI; 2002-171805/22.
 DR
 DR N-PSDB; ABK33872.
 XX
 PT Nucleic acids encoding lipase enzymes which are useful as supplements in
 PT animal feeds, as agents of flavor modification and for treating Crohn's
 PT disease and celiac disease.
 XX
 PS Claim 5; Page 145-146; 196pp; English.
 XX
 CC The invention relates to new Bacillus lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in

CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
 CC polypeptides of the invention
 XX
 SQ Sequence 180 AA;

Query Match 98.3%; Score 923; DB 5; Length 180;
 Best Local Similarity 97.8%; Pred. No. 2.7e-85;
 Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EHNPPVVMVHGIGGASFNPAIGIKSYLVSGWSRGKLYAVDFWDKTGTNTNNGPVLRSFVK 60
 DB 1 EHNPPVVMVHGIGGASFNPAIGIKSYLVSGWSRGKLYAVDFWDKTGTNTNNGPVLRSFVK 60
 QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLGGKNKVENVTLLGGTNRSTTSKALPGTDPNQ 120
 DB 61 VLDETGAKKVDIVAHSMGGANTLYIKNLGGKNKVENVTLLGGTNRSTTSKALPGTDPNQ 120
 QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
 DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

RESULT 7
 AAU83873
 ID AAU83873 standard; protein; 180 AA.
 AC AAU83873;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Bacillus lipase polypeptide #33.
 XX
 KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
 XX
 OS Synthetic.
 XX
 FN WO200206457-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 13-JUL-2001; 2001WO-US022160.
 XX
 PR 13-JUL-2000; 2000US-0217954P.
 PR 21-JUN-2001; 2001US-0300378P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 XX Giver LJ, Minshull J, Vogel K;
 PI
 XX WPI; 2002-171805/22.
 DR
 DR N-PSDB; ABK33851.
 XX
 PT Nucleic acids encoding lipase enzymes which are useful as supplements in
 PT animal feeds, as agents of flavor modification and for treating Crohn's
 PT disease and celiac disease.
 XX
 PS Claim 5; Page 143; 196pp; English.
 XX
 CC The invention relates to new Bacillus lipase enzymes and the nucleic

CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention
XX
SQ Sequence 180 AA;

Query Match 98.2%; Score 922; DB 5; Length 180;
Best Local Similarity 97.2%; Pred. No. 3.5e-85;
Matches 175; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EHNPMVVMHIGGASFNFAIGKSYLVSGWSRGKLYAVDFWDTGTNNYNGPVLRSFVKK 60
Db 1 EHNPMVVMHIGGASFNFAIGKSYLVSGWSRGKLYAVDFWDTGTNNYNGPVLRSFVKK 60

Qy 61 VLDETGAKKVDIVAHSMGGANTLYIYIKNLDDGKNKVENVTGLGTNRSTTSKALPGTDPNQ 120
Db 61 VLDETGAKKVDIVAHSMGGANTLYIYIKNLDDGKNKVENVTGLGTNRSTTSKALPGTDPNQ 120

Qy 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
Db 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

RESULT 8
AAU83863
ID AAU83863 standard; protein; 180 AA.
XX
AC AAU83863;
XX
DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polypeptide #23.
XX
KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuffs; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW gastrointestinal.
XX
OS Synthetic.
XX
FN WO200206457-A2.
XX
PD 24-JAN-2002.
XX
PF 13-JUL-2001; 2001WO-US022160.
XX
PR 13-JUL-2000; 2000US-0217954P.
PR 21-JUN-2001; 2001US-0300378P.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Giver LJ, Minshull J, Vogel K;
XX
DR WPI; 2002-171805/22.
DR N-PSDB; ABK3841.
XX
PT Nucleic acids encoding lipase enzymes which are useful as supplements in
PT animal feeds, as agents of flavor modification and for treating Crohn's
PT disease and coeliac disease.
XX
PS Claim 5; Page 141; 196pp; English.

CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention
XX
SQ Sequence 180 AA;

Query Match 98.0%; Score 920; DB 5; Length 180;
Best Local Similarity 97.2%; Pred. No. 5.5e-85;
Matches 175; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EHNPMVVMHIGGASFNFAIGKSYLVSGWSRGKLYAVDFWDTGTNNYNGPVLRSFVKK 60
Db 1 EHNPMVVMHIGGASFNFAIGKSYLVSGWSRGKLYAVDFWDTGTNNYNGPVLRSFVKK 60

Qy 61 VLDETGAKKVDIVAHSMGGANTLYIYIKNLDDGKNKVENVTGLGTNRSTTSKALPGTDPNQ 120
Db 61 VLDETGAKKVDIVAHSMGGANTLYIYIKNLDDGKNKVENVTGLGTNRSTTSKALPGTDPNQ 120

Qy 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
Db 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

RESULT 9
AAU83845
ID AAU83845 standard; protein; 212 AA.
XX
AC AAU83845;
XX
DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polypeptide #5.
XX
KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuffs; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW gastrointestinal.
XX
OS Bacillus circulans.
XX
FN WO200206457-A2.
XX
PD 24-JAN-2002.
XX
PF 13-JUL-2001; 2001WO-US022160.
XX
PR 13-JUL-2000; 2000US-0217954P.
PR 21-JUN-2001; 2001US-0300378P.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Giver LJ, Minshull J, Vogel K;
XX
DR WPI; 2002-171805/22.
DR N-PSDB; ABK3823.
XX
PT Nucleic acids encoding lipase enzymes which are useful as supplements in
PT animal feeds, as agents of flavor modification and for treating Crohn's
PT disease and coeliac disease.
XX
PS Claim 20; Page 139; 196pp; English.

XX The invention relates to new Bacillus lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in
 CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
 CC polypeptides of the invention
 XX
 SQ Sequence 212 AA;

Query Match 98.0%; Score 920; DB 5; Length 212;
 Best Local Similarity 97.2%; Pred. No. 6.9e-85;
 Matches 175; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EHNPMVMVHGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTNNNGPVLRSFVKK 60
 DB 33 EHNPMVMVHGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTNNNGPVLRSFVKK 92
 QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTLGTTNRSTTSKALPGTDPNQ 120
 DB 93 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTLGTTNRSTTSKALPGTDPNQ 152
 QY 121 KILYTSIYSSADMIVMNYLSKLDGAKVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
 DB 153 KILYTSIYSSADMIVMNYLSKLDGAKVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 212

RESULT 10
 AAU83844
 ID AAU83844 standard; protein; 212 AA.
 XX
 AC AAU83844;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Bacillus lipase polypeptide #4.
 XX
 KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
 KW gastrointestinal.
 XX
 OS Bacillus lentus.
 XX
 PN WO200206457-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 13-JUL-2001; 2001WO-US022160.
 XX
 PR 13-JUL-2000; 2000US-0217954P.
 PR 21-JUN-2001; 2001US-0300378P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 PI Giver LJ, Minshull J, Vogel K;
 XX
 DR WPI; 2002-171805/22.
 DR N-PSDB; ABK33822.
 XX
 PT Nucleic acids encoding lipase enzymes which are useful as supplements in
 PT animal feeds, as agents of flavor modification and for treating Crohn's
 PT disease and celiac disease.
 PT

PS Claim 20; Page 138-139; 196pp; English.
 XX The invention relates to new Bacillus lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in
 CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
 CC polypeptides of the invention
 XX
 SQ Sequence 212 AA;

Query Match 98.0%; Score 920; DB 5; Length 212;
 Best Local Similarity 97.2%; Pred. No. 6.9e-85;
 Matches 175; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EHNPMVMVHGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTNNNGPVLRSFVKK 60
 DB 33 EHNPMVMVHGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTNNNGPVLRSFVKK 92
 QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTLGTTNRSTTSKALPGTDPNQ 120
 DB 93 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTLGTTNRSTTSKALPGTDPNQ 152
 QY 121 KILYTSIYSSADMIVMNYLSKLDGAKVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
 DB 153 KILYTSIYSSADMIVMNYLSKLDGAKVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 212

RESULT 11
 AAU83885
 ID AAU83885 standard; protein; 180 AA.
 XX
 AC AAU83885;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Bacillus lipase polypeptide #45.
 XX
 KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
 KW gastrointestinal.
 XX
 OS Synthetic.
 XX
 PN WO200206457-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 13-JUL-2001; 2001WO-US022160.
 XX
 PR 13-JUL-2000; 2000US-0217954P.
 PR 21-JUN-2001; 2001US-0300378P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 PI Giver LJ, Minshull J, Vogel K;
 XX
 DR WPI; 2002-171805/22.
 DR N-PSDB; ABK33863.
 XX
 PT Nucleic acids encoding lipase enzymes which are useful as supplements in
 PT animal feeds, as agents of flavor modification and for treating Crohn's
 PT disease and celiac disease.
 PT

XX PS Claim 5; Page 144; 196pp; English.

XX CC The invention relates to new Bacillus lipase enzymes and the nucleic

XX CC acids encoding them. The lipase polypeptides are useful as supplements in

XX CC animal feeds, as agents of flavour modification and fat modification in

XX CC human foodstuffs (e.g. cheese), as agents in the creation of food

XX CC emulsifiers, as agents for tanning/processing of leather and as cleaning

XX CC agents. They are also useful for treating Crohn's disease, cystic

XX CC fibrosis, coeliac disease, indigestion, obesity and other

XX CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related

XX CC conditions can be therapeutically or prophylactically treated via a

XX CC method of hydrolysing a lipid comprising expressing in a target cell or

XX CC contacting a target cell with an effective amount of DNA or protein of

XX CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase

XX CC polypeptides of the invention

XX CC Sequence 180 AA;

SQ Query Match 97.9%; Score 919; DB 5; Length 180;

Best Local Similarity 97.2%; Pred. No. 7e-85; 2; Indels 0; Gaps 0;

Matches 175; Conservative 3; Mismatches 2;

QY 1 EHNPMVMVHGIGGASFNFAGIKSVLVSQGSRGKLYAVDFWDTGTNNNGPVLRSFVK 60

DB 1 EHNPMVMVHGIGGASFNFAGIKSVLVSQGSRGKLYAVDFWDRGTNNNGPVLRSFVK 60

QY 61 VLDETGAKKVDIVAHSMGGANTLYIYIKNLGGKNKVENVTILGGTNRSTTSKALPGTDPNQ 120

DB 61 VLDETGAKKVDIVAHSMGGANTLYIYIKNLGGKNKIENVTILGGANRSTTSKALPGTDPNQ 120

QY 121 KILYTSIYSSADMIWMVYLSKLDGAKNQIHGVGHIGLLMNSQVNSLIKEGLNGGGGLNTN 180

DB 121 KILYTSIYSSADMIWMVYLSKLDGAKNQIHGVGHIGLLMNSQVNSLIKEGLNGGGHNTN 180

RESULT 12

AAU83868

ID AAU83868 standard; protein; 180 AA.

XX AC AAU83868;

XX DT 08-MAY-2002 (first entry)

XX DE Bacillus lipase polypeptide #28.

XX KW Lipase; Bacillus; animal feed; flavour modification; fat modification;

XX KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;

XX KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;

XX KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;

XX KW gastrointestinal lipid related condition; antiinflammatory; respiratory;

XX KW Gastrointestinal.

XX OS Synthetic.

XX PN WO200206457-A2.

XX PD 24-JAN-2002.

XX PF 13-JUL-2001; 2001WO-US022160.

XX PR 13-JUL-2000; 2000US-0217954P.

XX PR 21-JUN-2001; 2001US-0300378P.

XX PA (MAXY-) MAXYGEN INC.

XX PI Giver LJ, Minshull J, Vogel K;

XX WPI; 2002-171805/22.

XX DR N-PSDB; ABK3846.

XX PT Nucleic acids encoding lipase enzymes which are useful as supplements in

XX PT animal feeds, as agents of flavor modification and for treating Crohn's

PT disease and celiac disease.

XX Claim 7; Page 142; 196pp; English.

XX CC The invention relates to new Bacillus lipase enzymes and the nucleic

XX CC acids encoding them. The lipase polypeptides are useful as supplements in

XX CC animal feeds, as agents of flavour modification and fat modification in

XX CC human foodstuffs (e.g. cheese), as agents in the creation of food

XX CC emulsifiers, as agents for tanning/processing of leather and as cleaning

XX CC agents. They are also useful for treating Crohn's disease, cystic

XX CC fibrosis, coeliac disease, indigestion, obesity and other

XX CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related

XX CC conditions can be therapeutically or prophylactically treated via a

XX CC method of hydrolysing a lipid comprising expressing in a target cell or

XX CC contacting a target cell with an effective amount of DNA or protein of

XX CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase

XX CC polypeptides of the invention

XX CC Sequence 180 AA;

SQ Query Match 97.7%; Score 917; DB 5; Length 180;

Best Local Similarity 96.7%; Pred. No. 1.1e-84; 2; Indels 0; Gaps 0;

Matches 174; Conservative 4; Mismatches 2;

QY 1 EHNPMVMVHGIGGASFNFAGIKSVLVSQGSRGKLYAVDFWDTGTNNNGPVLRSFVK 60

DB 1 EHNPMVMVHGIGGASFNFAGIKSVLVSQGSRGKLYAVDFWDTGTNNNGPVLRSFVK 60

QY 61 VLDETGAKKVDIVAHSMGGANTLYIYIKNLGGKNKVENVTILGGTNRSTTSKALPGTDPNQ 120

DB 61 VLDETGAKKVDIVAHSMGGANTLYIYIKNLGGKNKIENVTILGGANRSTTSKALPGTDPNQ 120

QY 121 KILYTSIYSSADMIWMVYLSKLDGAKNQIHGVGHIGLLMNSQVNSLIKEGLNGGGGLNTN 180

DB 121 KILYTSIYSSADMIWMVYLSKLDGAKNQIHGVGHIGLLMNSQVNSLIKEGLNGGGGLNTN 180

RESULT 13

AAU83893

ID AAU83893 standard; protein; 180 AA.

XX AC AAU83893;

XX DT 08-MAY-2002 (first entry)

XX DE Bacillus lipase polypeptide #53.

XX KW Lipase; Bacillus; animal feed; flavour modification; fat modification;

XX KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;

XX KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;

XX KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;

XX KW gastrointestinal lipid related condition; antiinflammatory; respiratory;

XX KW Gastrointestinal.

XX OS Synthetic.

XX PN WO200206457-A2.

XX PD 24-JAN-2002.

XX PF 13-JUL-2001; 2001WO-US022160.

XX PR 13-JUL-2000; 2000US-0217954P.

XX PR 21-JUN-2001; 2001US-0300378P.

XX PA (MAXY-) MAXYGEN INC.

XX PI Giver LJ, Minshull J, Vogel K;

XX WPI; 2002-171805/22.

XX DR N-PSDB; ABK3891.

XX PT Nucleic acids encoding lipase enzymes which are useful as supplements in

PT animal feeds, as agents of flavor modification and for treating Crohn's
PT disease and coliac disease.
XX
XX
PS Claim 5; Page 145; 196pp; English.
XX
CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention
XX
XX
SQ Sequence 180 AA;
Query Match 97.7%; Score 917; DB 5; Length 180;
Best Local Similarity 97.8%; Pred. No. 1.1e-84;
Matches 176; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 EHNPFVVMVHGIGGASFNFAGIKSVLSQGSRSKLYAVDFWDKGTNNYNGPVLRSFVKK 60
DB 1 EHNPFVVMVHGIGGASFNFAGIKSVLSQGSRSKLYAVDFWDKGTNNYNGPVLRSFVKK 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLGGNKVENVVTLLGGTNRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLGGNKVENVVTLLGGTNRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
RESULT 14
AAU83888
ID AAU83888 standard; protein; 180 AA.
XX
XX
AC AAU83888;
XX
DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polypeptide #48.
XX
KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW Gastrointestinal.
XX
OS Synthetic.
XX
XX WO200206457-A2.
XX
XX 24-JAN-2002.
XX
XX 13-JUL-2001; 2001WO-US022160.
XX
XX 13-JUL-2000; 2000US-0217954P.
XX
XX 21-JUN-2001; 2001US-0300378P.
XX
XX (MAXY-) MAXYGEN INC.
XX
XX Giver LJ, Minshull J, Vogel K;
XX
XX WPI; 2002-171805/22.
XX
XX N-PSDB; ABK33866.

PT Nucleic acids encoding lipase enzymes which are useful as supplements in
PT animal feeds, as agents of flavor modification and for treating Crohn's
PT disease and coliac disease.
XX
XX
PS Claim 5; Page 145; 196pp; English.
XX
CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention
XX
XX
SQ Sequence 180 AA;
Query Match 97.3%; Score 914; DB 5; Length 180;
Best Local Similarity 96.7%; Pred. No. 2.2e-84;
Matches 174; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EHNPFVVMVHGIGGASFNFAGIKSVLSQGSRSKLYAVDFWDKGTNNYNGPVLRSFVKK 60
DB 1 EHNPFVVMVHGIGGASFNFAGIKSVLSQGSRSKLYAVDFWDKGTNNYNGPVLRSFVKK 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLGGNKVENVVTLLGGTNRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLGGNKVENVVTLLGGTNRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
RESULT 15
AAU83889
ID AAU83889 standard; protein; 180 AA.
XX
XX
AC AAU83889;
XX
DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polypeptide #49.
XX
KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW Gastrointestinal.
XX
OS Synthetic.
XX
XX WO200206457-A2.
XX
XX 24-JAN-2002.
XX
XX 13-JUL-2001; 2001WO-US022160.
XX
XX 13-JUL-2000; 2000US-0217954P.
XX
XX 21-JUN-2001; 2001US-0300378P.
XX
XX (MAXY-) MAXYGEN INC.
XX
XX Giver LJ, Minshull J, Vogel K;
XX
XX WPI; 2002-171805/22.
XX
XX N-PSDB; ABK33867.

XX Nucleic acids encoding lipase enzymes which are useful as supplements in
PT animal feeds, as agents of flavor modification and for treating Crohn's
PT disease and celiac disease.
XX
PS Claim 5; Page 145; 196pp; English.
XX
CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, celiac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention
XX
SQ Sequence 180 AA;

Query Match 97.2%; Score 913; DB 5; Length 180;
Best Local Similarity 97.2%; Pred. No. 2.8e-84;
Matches 175; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 EHNPMVYHVGIGGASFNFAGIKSVLSQGRSGKLYAVDFWDKTGTNYNNGPVLSRFVKK 60
DB 1 EHNPMVYHVGIGGASFNFAGIKSVLSQGRSGKLYAVDFWDKTGTNYNNGPVLSRFVKK 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLGDNKVENNVTLGGTNRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLGDNKVENNVTLGGTNRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMVYNYLSKLDGAKNVOIHGVGHIGLLMNSQVNSLIKEGLNGGQNTN 180
DB 121 KILYTSIYSSADMVYNYLSKLDGAKNVOIHGVGHIGLLMNSQVNSLIKEGLNGGQNTN 180

Search completed: April 23, 2004, 10:11:56
Job time : 47.3776 secs